

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: July 22, 2006, 03:24:41 ; Search time 300 Seconds
(without alignments)
1476.942 Million cell updates/sec

Title: US-10-713-648A-63

Perfect score: 2534
Sequence: 1 MSSSATVPLVPLAYGNTSASV.....GENTDVTXKHSDAAPVTV 479

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_7.2.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2527	99.7	479	2	Q85IM9_ORYSA	Q85IM9 oryza sativ
2	2216	87.5	470	2	Q6T8L6_WHEAT	Q6T8L6 triticum ae
3	1991.5	78.6	498	2	Q84KJ6_ORYSA	Q84KJ6 oryza sativ
4	1889	74.5	480	2	Q69T29_ORYSA	Q69T29 oryza sativ
5	1871.5	73.9	486	2	Q93X02_ORYSA	Q93X02 lotus japon
6	1861	73.4	494	2	Q8H251_MEDTR	Q8H251 medicago tr
7	1715.5	67.7	497	2	Q8S233_ORYSA	Q8S233 oryza sativ
8	1714	67.6	486	2	Q84KJ7_ORYSA	Q84KJ7 oryza sativ
9	1714	67.6	486	2	Q84KJ5_ORYSA	Q84KJ5 oryza sativ
10	1687.5	66.6	497	2	Q8S230_ORYSA	Q8S230 oryza sativ
11	1682.5	66.4	475	1	AMT2_ARATH	Q9M677 arabidopsis
12	1436	56.7	458	2	Q2QY79_ORYSA	Q2QY79 oryza sativ
13	1297	51.2	359	2	Q3EBK4_ARATH	Q3EBK4 arabidopsis
14	1030	40.6	326	2	Q2RBN4_ORYSA	Q2RBN4 oryza sativ
15	1023.5	40.4	518	2	Q974J8_SULFO	Q974J8 sulfolobus
16	992.5	39.2	493	2	Q4JAD2_SULFO	Q4JAD2 sulfolobus
17	985.5	38.9	509	2	Q97275_SULFO	Q97275 sulfolobus
18	930.5	36.7	465	2	Q41R28_ERARC	Q41R28 ferropilasma
19	912.5	36.0	432	2	Q6K206_PICTO	Q6K206 picophyllus
20	722	28.5	412	1	Y663_METTH	Q6K206 picophyllus
21	720.5	28.4	446	2	Q7H2G8_THET2	Q7H2G8 thermus the
22	717.5	28.3	446	2	Q9HTR7_PSEAE	Q9HTR7 pseudomonas
23	709.5	28.0	445	2	Q5SM87_THET8	Q5SM87 thermus the
24	708.5	28.0	299	2	Q8W300_ORYSA	Q8W300 oryza sativ
25	706	27.9	423	1	AMT_AQUAE	Q6G515 aquilex aeo
26	697	27.5	437	2	Q7MA87_WOLSU	Q7MA87 wolinnella s
27	695.5	27.4	510	2	Q3RYC8_RALME	Q3RYC8 raietonia m
28	694	27.4	450	2	Q5P470_AZOSE	Q5P470 azoarcus sp
29	693.5	27.3	407	2	Q2NGJ2_9EURY	Q2NGJ2 methanospa
30	692.5	27.3	445	2	Q88B15_PSEEM	Q88B15 pseudomonas
31	691.5	27.3	445	2	Q50B00_PSEUD	Q50B00 pseudomonas

32	691	27.3	431	2	Q66DR9_YERPS	Q66DR9 yerersinia ps
33	691	27.2	431	2	Q8ZC80_YERPE	Q8ZC80 yerersinia pe
34	690.5	27.2	438	2	Q3AFY9_CARHZ	Q3AFY9 carboxydobh
35	690.5	27.2	445	2	Q4GC08_PSE14	Q4GC08 pseudomonas
36	683.5	27.0	434	2	Q3XA12_MERFL	Q3XA12 methylobact
37	681	26.9	436	2	Q8Y2J2_RALSO	Q8Y2J2 raietonia s
38	681	26.9	432	2	Q3PB17_PARDE	Q3PB17 paracoccus
39	680	26.8	438	2	Q8RPM1_PSEST	Q8RPM1 pseudomonas
40	676.5	26.7	443	2	Q2XHU3_PSEPU	Q2XHU3 pseudomonas
41	676.5	26.7	443	2	Q88CE8_PSEPK	Q88CE8 pseudomonas
42	676.5	26.7	445	2	Q3K4R2_PSEDP	Q3K4R2 pseudomonas
43	676	26.7	468	2	Q8RP89_PRHOO	Q8RP89 azoarcus sp
44	676	26.7	513	2	Q476K9_RALEJ	Q476K9 raietonia e
45	672.5	26.5	443	2	Q6ND36_RHOPA	Q6ND36 rhodospseudo

ALIGNMENTS

RESULT 1	ID	Q85IM9_ORYSA	PRELIMINARY	PRT	479 AA.
AC	Q85IM9	Q85IM9			
DT	01-JUN-2003	integrated into UniProtKB/TREMBL.			
DT	01-JUN-2003	sequence version 1.			
DT	21-FEB-2006	entry version 12.			
DE		Putative ammonium transporter.			
GN		Name=OSJNB0042109.15;			
OS		Oryza sativa (japonica cultivar-group).			
OC		Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC		Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BOP clade;			
OC		Ehrhartoideae; Oryzaceae; Oryza.			
OX		NCBI_TaxID=3947;			
RN		[1]			
RP		NUCLEOTIDE SEQUENCE.			
RA		Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M.,			
RA		Overson II L.L., Teitelin T., Kim M.M., Bera J.J., Jin S.S.,			
RA		Padrosh D.W., Tallon L.J., Koo H., Ziemann V., Hsiao J., Blunt S.,			
RA		Vanaken S.S., Riedmuller S.B., Utecherback T.T., Feldlyum T.V.,			
RA		Yang Q.Q., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J.,			
RA		White O., Salzberg S.L., Fraser C.M.;			
RT		Oryza sativa chromosome 3 BAC OSJNB0042109 genomic sequence."			
RU		Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.			
RN		[2]			
RP		NUCLEOTIDE SEQUENCE.			
RA		Buell R.;			
RU		Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.			
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CC		EMBL; AC104487; AAC41130.1; -; Genomic_DNA.			
CC		Gramene; Q85IM9; -			
DR		GO: GO:0016020; C:membrane; IEA.			
DR		GO: GO:0008519; F:ammonium transporter activity; IEA.			
DR		GO: GO:0008510; P:transport; IEA.			
DR		InterPro: IPR001905; Ammonium_transp.			
DR		InterPro: IPR010256; RH_like_transp.			
DR		InterPro: IPR002229; RhesusRD.			
DR		PANTHER: PTHR11730; Ammonium_transp; 1.			
DR		Pfam: PF00909; Ammonium_transp; 1.			
DR		PRINTS: PR00342; RHESUSRD.			
DR		TIGRfam: TIGR00836; amc; 1.			
DR		SEQUENCE 479 AA; 50853 MW; E9145C542F4664A5 CRC64;			
QY		Query Match 99.7%; Score 2527; DB 2; Length 479;			
QY		Best Local Similarity 99.6%; Pred. No. 3; 1e-178;			
QY		Matches 477; Conservative 1; Mismatches 1; Indels 0; Gaps 0;			
DB		1 MSSSATVPLVPLAYGNTSASVADMLNKGDNAWQVLAATVVLGLQSVPEGLVVLVYGGVVKKKMA 60			
DB		1 MSSSATVPLVPLAYGNTSASVADMLNKGDNAWQVLAATVVLGLQSVPEGLVVLVYGGVVKKKMA 60			

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QY 61 VNSAFMAALYAPAAVMTICWVTMAVYNNMSFGEBKLPIWKGARPALDOGLVGRALPATVHR 120
DB 61 VNSAFMAALYAPAAVMTICWVTMAVYNNMSFGEBKLPIWKGARPALDOGLVGRALPATVHR 120
QY 121 ADGSVETAABEPLYPMAVTVVYFQCVPAATLLILVAGSLIGRMSFLAMMI FVPLMTFSYT 180
DB 121 ADGSVETAABEPLYPMAVTVVYFQCVPAATLLILVAGSLIGRMSFLAMMI FVPLMTFSYT 180
QY 181 VAFPSLWGGGFLFHHGVVDYCCGYVYHVSAGTAGFPAAYWGPRAQKDERPPNNILFT 240
DB 181 VAFPSLWGGGFLFHHGVVDYCCGYVYHVSAGTAGFPAAYWGPRAQKDERPPNNILFT 240
QY 241 LTGAGLLMGMAGFNGGPGYAAANSVASMALVNTNICTAMSLLVWTCLDVIFPKKSVGA 300
DB 241 LTGAGLLMGMAGFNGGPGYAAANSVASMALVNTNICTAMSLLVWTCLDVIFPKKSVGA 300
QY 301 VOGMITGLVCTIPPAAGVVOGMAALVWGLAGSIPWYTMWILHKRSKILQVDDTLGVFHT 360
DB 301 VOGMITGLVCTIPPAAGVVOGMAALVWGLAGSIPWYTMWILHKRSKILQVDDTLGVFHT 360
QY 361 HGVAGLLGGLLTGLFAEPTLCNLFLPVADSRGAFYGGAGAGQAFQKQIAGGLFVAMNVV 420
DB 361 HGVAGLLGGLLTGLFAEPTLCNLFLPVADSRGAFYGGAGAGQAFQKQIAGGLFVAMNVV 420
QY 421 TSLICLAIMLVPLRMPDDKLEVGDDAVHGEBAVALMGDEMYDTYKGSDAAPV 479
DB 421 TSLICLAIMLVPLRMPDDKLEVGDDAVHGEBAVALMGDEMYDTYKGSDAAPV 479

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RESULT 2

067816 WHEAT PRELIMINARY; PRT: 470 AA.

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AC 067816_1
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 1.
DE Ammonium transporter AMT2.1.
GN Name=AmT2.1.
OS Triticum aestivum (Wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Bep clade;
OC Poaceae; Triticeae; Triticum.
OX NCBI_TaxID=4565;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Zhao X., Yang G., Tong Y., Li B., Miao J., Li Z.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
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CC -----
EMBL: AY428038; AAR87397.1; -, mRNA.
DR Gramene; Q67816; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008519; F:ammonium transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR001905; Ammonium_transp.
DR InterPro; IPR001734; Na_solut_transp.
DR InterPro; IPR010256; RH_like_transp.
DR PANTHER; PTHR11730; Ammonium_transp.
DR Pfam; PF00909; Ammonium_transp; 1.
DR PRINTS; PR00343; RHESUSRD.
DR TIGRFAIR; TIGR00836; amc; 1.
DR PROSITE; PS00457; NA_SOLUT_SYM_2; UNKNOWN_1.
SQ SEQUENCE 470 AA; 50056 MW; 96804C139DC46A38 CRC64;

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Query Match 87.5%; Score 2216; DB 2; Length 470;
 Best Local Similarity 86.0%; Pred. No. 2.9e-155;
 Matches 404; Conservative 30; Mismatches 34; Indels 2; Gaps 1;

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DB 3 VPVAYQNTSAAVADWLNKGDNAQLTASLTGLMSVPGMNVVLYGGVKKKAAVNSAFMA 62
QY 68 LYAPAAVMTICWVTMAVYNNMSFGEBKLPIWKGARPALDOGLVGRALPATVHRADGSVET 127
DB 63 LYAPAAVMTICWVTMAVYNNMSFGEBKLPIWKGARPALDOGLVGRALPATVHRADGSVET 122
QY 128 AAVEPLYPMAVTVVYFQCVPAATLLILVAGSLIGRMSFLAMMI FVPLMTFSYTGAFLSW 187
DB 123 AMVEYFPMAVTVVYFQCVPAATLLILVAGSLIGRMSFLAMMI FVPLMTFSYTGAFLSW 182
QY 188 GGGFLFHHGVVDYCCGYVYHVSAGTAGFPAAYWGPRAQKDERPPNNILFTLTGAGLL 247
DB 183 GGGFLFHHGVVDYCCGYVYHVSAGTAGFPAAYWGPRAQKDERPPNNILFTLTGAGLL 242
QY 248 WGMAGFNGGPGYAAANSVASMALVNTNICTAMSLLVWTCLDVIFPKKSVGA VOGMITG 307
DB 243 WGMAGFNGGPGYAAANSVASMALVNTNICTAMSLLVWTCLDVIFPKKSVGA VOGMITG 302
QY 308 LVCTIPPAAGVVOGMAALVWGLAGSIPWYTMWILHKRSKILQVDDTLGVFHTGAGLL 367
DB 303 LVCTIPPAAGVVOGMAALVWGLAGSIPWYTMWILHKRSKILQVDDTLGVFHTGAGLL 362
QY 368 GGLLTGLFAEPTLCNLFLPVADSRGAFYGGAGAGQAFQKQIAGGLFVAMNVVYTSLICLA 427
DB 363 GGLLTGLFAEPTLCNLFLPVADSRGAFYGGAGAGQAFQKQIAGGLFVAMNVVYTSLICLA 422
QY 428 INLVPLRMPDDKLEVGDDAVHGEBAVALMGDEMYDTYKGSDAAPV 477
DB 423 INLVPLRMPDDKLEVGDDAVHGEBAVALMGDEMYDTYKGSDAAPV 470

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RESULT 3

084KJ6 ORYZA PRELIMINARY; PRT: 498 AA.

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AC 084KJ6_1
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.
DT 07-FEB-2006, entry version 8.
DE Ammonium transporter.
GN Name=OsAMT2;2.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Bep clade;
OC Ehrhartoideae; Oryzoae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA TISSUE=Root;
RX MEDLINE=22497958; PubMed=12610225; DOI=10.1093/pcp/pcg017;
RA Suenaga A., Moriya K., Sonoda Y., Ikeda A., von Widen N., Hayakawa T.,
RA Yamaguchi J., Yamaya T.;
RT "Constitutive expression of a novel-type ammonium transporter OsAMT2
RT in rice plants."
RL Plant Cell Physiol. 44:206-211(2003).
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CC -----
EMBL: AB083582; BAC65232.1; -, mRNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008519; F:ammonium transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR001905; Ammonium_transp.
DR InterPro; IPR010256; RH_like_transp.
DR PANTHER; PTHR11730; Ammonium_transp.
DR Pfam; PF00909; Ammonium_transp; 1.
DR TIGRFAIR; TIGR00836; amc; 1.
DR PROSITE; PS01219; AMMONIUM_TRANSP; 1.
SQ SEQUENCE 498 AA; 53794 MW; 974AC5F13D05E0 CRC64;

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Query Match 78.6%; Score 1991.5; DB 2; Length 498;
 Best Local Similarity 75.6%; Pred. No. 1.2e-138;
 Matches 359; Conservative 53; Mismatches 56; Indels 7; Gaps 3;

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QY 1 MSSATVPLAYOGNTSASVADMLKGDNAQOLVAATVGLQSVFGLVYLGGVKKKNA 60
DB 1 MSQDARNMSVAYQPSGMA-VPEWLNKGDNAQOMISATLVGMSQSPGLVILYGSIVKKKNA 59
QY 61 VNSAFALYAFPAVWICWTTAAYNMSFGEKLLPIWGKARPALDOGLLVGRALPATVHY- 119
DB 60 VNSAFALYAFPAVWICWTTAAYNMSFGEKLLPIWGKARPALDOGLLVGRALPATVHY- 119
QY 120 ---RADGSVETAAVEPLYPMATVYVYFQCFAAITLLVAGSLIGRMSFLAMMI FVPLML 175
DB 120 KGGGADAVAVETPMVPLVPMATMVTYFQCFAAITLLVAGSLIGRMINIKAMLFVPLML 179
QY 176 TTSYTTGAISLWGGGFLFHMGVVDYCGGYVYHISAGIAGTAAVYWGPRAKRERPPN 235
DB 180 TTSYTTGAISLWGGGFLFHMGVVDYCGGYVYHISAGIAGTAAVYWGPRAKRERPPN 239
QY 236 NILFTLTGAGLMMGNAGFNGGPRYANSVASMAVLTNTICTAMSLIWTCLDVIFPKKP 295
DB 240 NVLMLTGAIGLMMGNAGFNGGPRYSANIDSLAVLNTINCAATSLIWTCLDVIFPKKP 299
QY 296 SVGAVOGMITGLVCTTPAAGVVOGMAALVYVLAGSIPWYTMILHKRSKILQRYDDTL 355
DB 300 SVIAGVQMITGLVCTTPAGLVQGMALVYVLAGSIPWYTMVYVHKSRLILQYDDTL 359
QY 356 GVFTHTGAGLGLLTGLFAEPTLCNLFVPVDSRGAFY-GGAGAGQSGKQIAGLFPV 414
DB 360 GVFTHTGAGLGLLTGLFAEPTLCNLFVPVDSRGAFY-PGRGGIQLFRVQVAGALFII 419
QY 415 AMNVVYTSILCLAINLLVPLRMPDKLEVGDVAHGEBAVALMGDEMDVTYKHG 469
DB 420 CMNVVYTSILCLAINLLVPLRMPDEELIAGDDAVHGEBAVALMGDEMDVTYKHG 474

RESULT 4
Q69T29_ORYSA PRELIMINARY; PRT; 480 AA.
AC Q69T29;
DT 25-OCT-2004, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 1.
DE Putative ammonium transporter.
GN Name=P0451A10.33;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 2, PAC
clone: P0451A10."
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
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CC -----
EMBL: AP004775; BAD33268.1; -, Genomic_DNA.
DB Gramene; Q69T29;
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008519; F:ammonium transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR001905; Ammonium transp.
DR InterPro; IPR010256; RH like transp.
DR Panther; PTHR11730; Ammonium transp.; 1.
DR Pfam; PF00909; Ammonium transp.; 1.
DR PRINTS; PR00342; RHESUSRD.
DR TIGRfam; TIGR00836; amt; 1.
DR PROSITE; PS01219; AMMONIUM_TRANSP; 1.
SQ SEQUENCE 480 AA; 51660 MW; 2964439DACA5DA35 CRC64;

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Query Match 74.5%; Score 1889; DB 2; Length 480;
Best Local Similarity 72.0%; Pred No. 4.2e-131;
Matches 335; Conservative 62; Mismatches 66; Indels 2; Gaps 1;

QY 4 SATVPLAYOGNTSASVADMLKGDNAQOLVAATVGLQSVFGLVYLGGVKKKNAVS 63
DB 2 AAGATPMAYQ--TTSPSPMLKGDNAQMTSATVGLQSMFGVLVLYGSIVKKKNAVS 59
QY 64 AFMALYAFPAVWICWTTAAYNMSFGEKLLPIWGKARPALDOGLLVGRALPATVHYRAD 123
DB 60 AFMALYAFPAVWICWTTAAYNMSFGEKLLPIWGKARPALDOGLLVGRALPATVHYRAD 119
QY 124 SVETAVERPLYPMATVYVYFQCFAAITLLVAGSLIGRMSFLAMMI FVPLMLTFSYVGA 183
DB 120 SAEAPMLKPLYPMATVYVYFQCFAAITLLVAGSLIGRMINIKAMLFVPLMLTFSYVGA 179
QY 184 FSLWGGGFLFHMGVVDYCGGYVYHISAGIAGTAAVYWGPRAKRERPPNLIETLNG 243
DB 180 FSLWGGGFLFHMGVVDYCGGYVYHISAGIAGTAAVYWGPRASDRERPPNLIETLNG 239
QY 244 AGLMMGNAGFNGGPRYANSVASMAVLTNTICTAMSLIWTCLDVIFPKKSVGAVOG 303
DB 240 AGLMMGNAGFNGGPRYSANIDSMVAVLTNTICTASTLLVTLDFVFGKESVIGAVOG 299
QY 304 MTGLVCTTPAAGVVOGMAALVYVLAGSIPWYTMILHKRSKILQRYDDTLGVFTHTGY 363
DB 300 MTGLVCTTPAAGLVQGMALVYVLAGSIPWYTMVYVHKSRLILQYDDTLGVFTHTAV 359
QY 364 AGLGLGLTGLFAEPTLCNLFVPVDSRGAFYGGAGAGQIFGQIAGLFPVAMNVVYSL 423
DB 360 AGLGLGATGLFAEPTLCNLFVPVDSRGAFYGGAGAGQIFGQIAGLFPVAMNVVYSL 419
QY 424 ICLAINLLVPLRMPDKLEVGDVAHGEBAVALMGDEMDVTYKH 468
DB 420 ICYISILPLRLADQLIAGDDAVHGEBAVALMGDEMDVTYKH 464

RESULT 5
Q93X02_LOTUA PRELIMINARY; PRT; 486 AA.
AC Q93X02;
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 14.
DE Putative ammonium transporter AMT2.
OS Lotus japonicus.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteeae; Lotus.
OX NCBI_TaxID=34305;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA TISSUE=Nitrogen-fixing nodules;
RT TISSUE=Nitrogen-fixing nodules;
RX MEDLINE=22490499; PubMed=12602894; DOI=10.1023/A:1020710222298;
RA Simon-Rosin U., Wood C., Urdavari M.K.;
RT "Molecular and cellular characterisation of LjAMT2;1, an ammonium
transporter from the model legume Lotus japonicus."
RL Plant Mol. Biol. 51:99-108 (2003).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Nitrogen-fixing nodules;
RA Simon U., Urdavari M.K.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
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CC -----
EMBL: AF187962; AAL08212.1; -, mRNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008519; F:ammonium transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR001905; Ammonium transp.
DR InterPro; IPR010256; RH like transp.

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DR InterPro: IPR002229; RheusHRD.
DR PANTHER: PTHR11730; Ammonium_transpt; 1.
DR Pfam: PF00909; Ammonium_transp; 1.
DR PRINTS: PR00342; RHESUSHRD.
DR TIGRFAMs: TIGR00836; amc; 1.
DR PROSITE: PS01219; AMMONIUM_TRANSPT; 1.
SQ SEQUENCE 486 AA; 52343 MW; 060E893849FA334D CRC64;

Query Match 73.9%; Score 1871.5; DB 2; Length 486;
Best Local Similarity 73.6%; Pred. No. 8.3e-130;
Matches 340; Conservative 49; Mismatches 72; Indels 1; Gaps 1;

OY 9 PLAYGNTSASVADMLNKGNAMQLVAAATLVGQSVPGLVVLVYGGVKKKMAVNSAFMAL 68
DB 4 PLAYENLPAS-PEMLNKGDNAMQMTAATLVGLQSMGLVITLVAASYVESTHYFNNGSIETQ 62
OY 69 YAFAAVMICWVTAAVYNNMSEKLLPIWGKARPALDOGLVGRALPATVHYRADGSVETA 128
DB 63 YAFAAVLLCWVLICVRMARGDKLPFWGKAPALGQKFLINQASVESTHYFNNGSIETQ 122
OY 129 AVEPLPMATVYVFCVPAITLLVAGSLGRMSFLAMNIFVPLMTFSYTVGAFSLMG 188
DB 123 TORPEYPAATLVYFQFNFAITMILLAGSVLGRMNIKAMMAFVPLMLTFSYTVGAFSLMG 182
OY 189 GGFLEPMGVIDYCGGVYIHVSAGIAGFTAAVYWGPPRAQKDRERFPNNILFTLTGAGLLM 248
DB 183 GGFLEPMGVIDYSGGVYIHLSSGIAGFTAAVYWGPPRLKSDRERFPNNVLLMLAGAGLLM 242
OY 249 MGWAGFNGGPPYAANSVASMAVLTNTNICAMSLLVTCCLDVIFPKKPSVYGAQGMITGL 308
DB 243 MGWAGFNGGAPYAANIDASIAVLTNTNICATSLVWTSIDVAFGKPSYIGAQQMMTGL 302
OY 309 VQITPAAGVQGAALVWGLVAGSTIPWYTMILHKRSKLLQKVDLTGVFHTHAAGLLG 368
DB 303 VQITPAAGVQGAALVWGLVAGSTIPWYTMILHKRSKLLQKVDLTGVFHTHAAGLLG 362
OY 369 GLTGLFAEPTLCNLEPLPADSRGAFYGGAGAGQFQKQIAGGLFVYAMVWVTSILCLAI 428
DB 363 GLTGLFAEPTLCNLEPLPADSRGAFYGGAGAGQFQKQIAGGLFVYAMVWVTSILCLAI 422
OY 429 NLVPLRMPDDKLEVGDDAVHGEBAAYALWGDGEMVDVTHGS 470
DB 423 NLVPLRMPDDKLEVGDDAVHGEBAAYALWGDGEMVDVTHGS 464

RESULT 6
Q8H251_MEDTR PRELIMINARY; PRT; 494 AA.
ID Q8H251;
AC Q8H251;
DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 10.
DE Amc2-like protein.
OS Medicago truncatula (Barrel medic).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eusteroids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
OC Medicago.
OX NCBI_TaxID=3880;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Peng J., Chen Y., Huang C.-H.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
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CC -----
EMBL: AY123328; AAN06953.1; -; mRNA.
DR GO: GO:0016020; Cmembrane; IEA.
DR GO: GO:0008519; F:ammonium transporter activity; IEA.
DR InterPro: IPR001905; Ammonium_transpt.
DR InterPro: IPR010256; RH_like_transpt.
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DR InterPro: IPR002229; RheusHRD.
DR PANTHER: PTHR11730; Ammonium_transpt; 1.
DR Pfam: PF00909; Ammonium_transp; 1.
DR PRINTS: PR00342; RHESUSHRD.
DR TIGRFAMs: TIGR00836; amc; 1.
DR PROSITE: PS01219; AMMONIUM_TRANSPT; 1.
SQ SEQUENCE 494 AA; 53292 MW; D0F0816330ADD4F4 CRC64;

Query Match 73.4%; Score 1861; DB 2; Length 494;
Best Local Similarity 71.5%; Pred. No. 5e-129;
Matches 338; Conservative 55; Mismatches 74; Indels 6; Gaps 3;

OY 11 AYQNTSASVADMLNKGNAMQLVAAATLVGQSVPGLVVLVYGGVKKKMAVNSAFMAL 70
DB 6 AYQNLPLPS-PEMLNKGDNAMQMTAATLVGLQSMGLVITLVAASYVESTHYFNNGSIETQ 64
OY 71 FAAVMICWVTAAVYNNMSEKLLPIWGKARPALDOGLVGRALPATVHYRADG-SVEFDA 129
DB 65 FAAVLLICWVLVAYRMAFDELLPFWGKAPALGQKFLVBARAKVPASTHYXKGVDETQPM 124
OY 130 VEPLPMATVYVFCVPAITLLVAGSLGRMSFLAMNIFVPLMTFSYTVGAFSLMG 189
DB 125 BEPEPMASTLVYFQFTFAITMILLAGSVLGRMNIKAMMAFVPLMLTFSYTVGAFSLMG 184
OY 190 GGFLEPMGVIDYCGGVYIHVSAGIAGFTAAVYWGPPRAQKDRERFPNNILFTLTGAGLLM 249
DB 185 GGFLEPMGVIDYSGGVYIHLSSGIAGFTAAVYWGPPRLKSDRERFPNNVLLMLAGAGLLM 244
OY 250 MGWAGFNGGPPYAANSVASMAVLTNTNICAMSLLVTCCLDVIFPKKPSVYGAQGMITGL 309
DB 245 MGWAGFNGGAPYAANVASIAVLTNTNICATSLVWTSIDVAFGKPSYIGAQQMMTGL 304
OY 310 CITPAAGVQGAALVWGLVAGSTIPWYTMILHKRSKLLQKVDLTGVFHTHAAGLLG 369
DB 305 CITPAAGVQGAALVWGLVAGSTIPWYTMILHKRSKLLQKVDLTGVFHTHAAGLLG 364
OY 370 LITGLFAEPTLCNLEPLPADSRGAFYGGAGAGQFQKQIAGGLFVYAMVWVTSILCLAI 429
DB 365 LITGLFAEPTLCNLEPLPADSRGAFYGGAGAGQFQKQIAGGLFVYAMVWVTSILCLAI 424
OY 430 NLVPLRMPDDKLEVGDDAVHGEBAAYALWGDGEMVDVTHGS---DAVAPV 478
DB 425 LPIPLRMPDEQLIEIGDDAAGEBAAYALWGDGEXYPTBHSINTGTVSPV 477

RESULT 7
Q8S233_ORYSA PRELIMINARY; PRT; 497 AA.
ID Q8S233;
AC Q8S233;
DT 01-JUN-2002, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 15.
DE Putative ammonium transporter.
GN Name=P044604.35;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BBP clade;
OC Eriocaridaceae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22337376; PubMed=12447438; DOI=10.1038/nature01184;
RA Saeki T., Matsunoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,
RA Wu J., Nishimura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,
RA Hosokawa S., Masuoka M., Arikawa K., Chiden Y., Hayashi M.,
RA Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,
RA Hishida S., Honda M., Ichikawa Y., Idonuma A., Iijima M., Ikeda M.,
RA Ikono M., Ito S., Ito Y., Ito Y., Iwabuchi A., Kamiya K.,
RA Karasawa M., Katagiri S., Kikuta A., Kobayashi N., Kono I.,
RA Nachita K., Maehara T., Mizuno H., Mizubayashi T., Mukai Y.,
RA Nagasaki K., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M.,
RA Namiki N., Negishi M., Ohta I., Ono N., Saji S., Sakai K., Shibata M.,
RA Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Tsuji K.,
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CC Eubacteriaceae; Oryzaeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Roots;
RX MEDLINE=22497958; PubMed=12610225; DOI=10.1093/pcp/pcg017;
RA Suenaga A., Moriya K., Sonoda Y., Ikeda A., von Wiren N., Hayakawa T.,
RA Yamaguchi J., Yamaya T.;
RT "Constitutive expression of a novel-type ammonium transporter OsAMT2
in rice plants.";
RL Plant Cell Physiol. 44:206-211(2003).
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CC -----
CC EMBL; AB051864; BAB87832.1; -; mRNA.
DR Gramene; Q84K95; -
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008059; F:ammonium transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR019051; Ammonium transpct.
DR InterPro; IPR010256; RH like transpct.
DR InterPro; IPR002229; RhesusRD.
DR PANTHER; PTHR11730; Ammonium transpct; 1.
DR Pfam; PF00909; Ammonium transp; 1.
DR PRINTS; PR00342; RHESUSRD.
DR TIGRFAMs; TIGR00836; ant; 1.
DR PROSITE; PS01219; AMMONIUM_TRANSF; 1.
SQ SEQUENCE 486 AA; 51411 MW; D7084292E8CB7E7 CRC64;

Query Match 67.6%; Score 1714; DB 2; Length 486;
Best Local Similarity 69.0%; Pred. No. 3.5e-118;
Matches 319; Conservative 51; Mismatches 82; Indels 10; Gaps 4;

QY 10 LAYQGNISAS---VADMLNKDNAMQVAAITVLGASVPGILVVLGGVKKKMAVNSAFM 66
DB 1 MAAAGASASLPAVPMDLNKGDNAHQTAISLTVIGSMPLGVVLVYGSIVKKMAVNSAFM 60

QY 67 ALVAPAAVWICWTWAVNMSFGKELPIWKGARPALDQGLIVRAALPATVHYRADGSVE 126
DB 61 ALVAYASSLLVWVLVGRMAFGDQLPFWGAGVALQSYLVGRATLPATAH---GAI- 115

QY 127 TAATVEPLYPAAVTVVPCQVPAITLLI VAGSLGRMSFLAMFI PVPLMLPFSYVGAFSL 186
DB 116 -PRTEPPYPEPTLTLVFOFEPAALITLVLAGSVLGRMKIKAMMAETPEMLLSYVGAFSL 174

QY 187 WGGFELPHMGIVIDCGGVIVHSAGIAGFTAAVWVGPAQKDRERFPNNILFTLVAGL 246
DB 175 WGGFELTRMGVIDVSGGVVHLHSGIAGFTAAVWVGRLKSDRRERFPNNILMIAGGL 234

QY 247 LMMMGAFNGGPGPYAANSVASMALVNTNICTAMSLVWTCLDVIFPKKPSVYVAGVQMIT 306
DB 235 LMMMGAFNGGAPYAAVIAASVAVLNTNVCAATSLMWTCLDVIFPKKPSVYVAGVQMIT 294

QY 307 GLVCIITPAAGVYVGMALVWGVLAGSLPWTYMTLLHRSKTLQAVDDTLGFIHTHVAAGL 366
DB 295 GLVCIITPGAGIVQYMAAVVMGIFPGSVPMFMMLIHKSALMLMKVDDTLVAFHTHVAAGL 354

QY 367 LGGILTLGLPAEPTLCNLEFLPADSRGAFYGGAGAGQFGKQIAGGLFVAAVNVVTSILCL 426
DB 355 LGGILTLGLALTPELFSLESTVPGRLKGFYGG-GIKQIGKQUGAAAFVIAVNVVTTAILL 413

QY 427 AINLLVPLRMPDDKLEVGDDAVHGEAAVYALMGDEMYDVTKH 468
DB 414 GIGLFIPLRMPDDEQIMIGDDAAHGEAAVYALMGDEKEDATRH 455

RESULT 9
OS84KJ7_ORYZA PRELIMINARY; PRT; 486 AA.
AC OS84KJ7;
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.

07-FEB-2006, entry version 12.
 DE Ammonium transporter.
 GN Name=OsAMT2; Synonyms=OJ1058-C01.9;
 OS Oryza sativa (Japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BFP clade;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 NCBI_TaxId=399477;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Etioolated shoot;
 RX MEDLINE=22497958; PubMed=12610225; DOI=10.1093/pcp/pcg017;
 RA Suenaga A., Moriya K., Sonoda Y., Ikeda A., von Wieren N., Hayakawa T.,
 RA Yamaguchi J., Yamaya T.;
 RT "Constitutive expression of a novel-type ammonium transporter OsAMT2
 in rice plants."
 RL Plant Cell Physiol. 44:206-211(2003).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Chow T.-Y., Hsing Y.-I.C., Chen C.-S., Chen H.-H., Liu S.-M.,
 RA Chao Y.-T., Chang S.-J., Chen H.-C., Chen S.-K., Chen T.-R.,
 RA Hsing J.-L., Cheng C.-H., Chung C.-I., Han S.-Y., Hsiao S.-H.,
 RA Hsiung J.-N., Hsu C.-H., Huang J.-J., Kau P.-I., Lee M.-C., Liu H.-L.,
 RA Li Y.-F., Lin S.-J., Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W.,
 RA Wu H.-P., Shaw J.-F.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
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 CC EMBL AB083581, BAC65231.1; -; Genomic DNA.
 DR EMBL, AC113159; AAT47008.1; -; Genomic DNA.
 DR Gramene; Q84KJ7;
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0008519; F:ammonium transporter activity; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR001905; Ammonium transp.
 DR InterPro; IPR010256; RH like transp.
 DR InterPro; IPR002229; RheusRHD.
 DR PANTHER; PTHR11730; Ammonium transp.; 1.
 DR Pfam; PF00909; Ammonium transp.; 1.
 DR PRINTS; PR00342; RHESUSRHD.
 DR TIGRFAMs; TIGR00836; amc; 1.
 DR PROSITE; PS01219; AMMONIUM TRANSP.; 1.
 SQ SEQUENCE 486 AA; 51411 MW; D70842B92B8CB7E7 CRC64;
 Query Match 67.6%; Score 1714; DB 2; Length 486;
 Best Local Similarity 69.0%; Pred. No. 3,5e-118;
 Matches 319; Conservative 51; Mismatches 82; Indels 10; Gaps 4;
 QY 10 LAYGNTSAS---VADWLKKGDNAMQVLAATLVGLQSVGLVVLVYGVVKKKKAANSAM 66
 DB 1 MAAAGYSASLPAVPMLNKGDMAMQLTASTLVGISMPGLVVLVYGVVKKKKAANSAM 60
 QY 67 ALYAFAPAVVICWWTAYNNMSFGKELPIWGKAPALDOGLVGRALPATVHYRADSYE 126
 DB 61 ALYAYSSSLVWLVGFRAFGDQLPFGKAGVALTOSTVGRATLPATAH---GAI- 115
 QY 127 TAAYEELPMATVYVQCFAATLLILVAGSLGRNSFLAMMIFVBLMTFSYTVAGFSL 186
 DB 116 -PRTEPFYEATLVLFQFEPAATITLVLAGSVLGRNNIKAMMAFTPLLSTYVGAFFSL 174
 QY 187 WGGGFLFHHGVLDYCGGYIHSAGTAGTAAVWGPRAOKDREPPNNILFTLTGAGL 246
 DB 175 WGGGFLYRWGVLDYSGGYIHSAGTAGTAAVWGPRAOKDREPPNNILMTAGGGL 234
 QY 247 LMMGMAFGNGGPGYANVSAMVNLNTNICTAMSLVMTCLDVIFPKKSSVGAOGMIT 306
 DB 235 LMMGMAFGNGGPGYANVAINASAVLNTNVCATSLMTCLDVIFPKKSSVGAOGMIT 294
 QY 307 GLVCITPAAGVVGMAALVWGLAGSI PMYTMMLHKRSKILQKRVDDTLGVFTHGAVGL 366
 DB 295 GLVCITPAAGVVGMAALVWGLAGSI PMYTMMLHKRSKILQKRVDDTLGVFTHGAVGL 354

QY 367 IGGLTGLFAEPTLCNLFPAVDSRGAFYGGAGAGOFKQIAGGLFVYANNVVTSLICL 426
 DB 335 IGGITGLTATPELFSLSESTYPGLRGAFYGG-GIKQIKQKQAGAAFYANMLVTTALL 413
 QY 427 AINLVLPMPDDKLEVGDDAVHGEAYALWGDSEMYDVTH 468
 DB 414 GIGLFIPLRMPDEQLMGDDAAHGEAYALWGDSEKFPATRH 455
 RESULT 10
 OS O85230 ORYSA
 ID O85230 ORYSA PRELIMINARY; PRT; 497 AA.
 AC O85230;
 DT 01-JUN-2002, integrated into UniProtKB/TrEMBL.
 DT 01-JUN-2002, sequence version 1.
 DE 07-FEB-2006, entry version 15.
 GN Name=OsAMT2; Synonyms=OJ1058-C01.9;
 OS Oryza sativa (Japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BFP clade;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 NCBI_TaxId=399477;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22337376; PubMed=12447438; DOI=10.1038/nature01184;
 RA Sasaki T., Matsunoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,
 RA Wu Y., Nilmura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanemori H.,
 RA Hosokawa S., Masukawa M., Arikawa K., Chiden Y., Hayashi M.,
 RA Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,
 RA Hijiwata S., Honda M., Ichikawa Y., Idonuma A., Iijima M., Ikeda M.,
 RA Ikono M., Ito S., Ito T., Ito Y., Iwabuchi A., Kamiya K.,
 RA Katsawa M., Katagiri S., Kikuta A., Kobayashi N., Kono I.,
 RA Machita K., Maehara T., Mizuno H., Mizudayashi T., Mukai Y.,
 RA Nagasaki H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M.,
 RA Namiki N., Negishi M., Ohta I., Ono N., Saji S., Sakai K., Shibata M.,
 RA Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Teuji K.,
 RA Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K.,
 RA Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.-I., Eun M.-Y.,
 RA Yano M., Jiang J., Gojobori T.;
 RT "The genome sequence and structure of rice chromosome 1."
 RL Nature 420:312-316(2002).
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 CC EMBL, AP003252; BAB89598.1; -; Genomic DNA.
 DR Gramene; Q8S230;
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0008519; F:ammonium transporter activity; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR010256; Ammonium transp.
 DR InterPro; IPR002229; RheusRHD.
 DR PANTHER; PTHR11730; Ammonium transp.; 1.
 DR Pfam; PF00909; Ammonium transp.; 1.
 DR PRINTS; PR00342; RHESUSRHD.
 DR TIGRFAMs; TIGR00836; amc; 1.
 DR PROSITE; PS01219; AMMONIUM TRANSP.; 1.
 SQ SEQUENCE 497 AA; 53202 MW; 909D3CF41508C93B CRC64;
 Query Match 66.6%; Score 1887.5; DB 2; Length 497;
 Best Local Similarity 67.7%; Pred. No. 3.3e-116;
 Matches 304; Conservative 54; Mismatches 90; Indels 1; Gaps 1;
 QY 19 SVADNLKNGDNAMQVLAATLVGLQSVGLVVLVYGVVKKKKAANSAPALYAFAPAVVICW 78
 DB 16 AVPAALNKGDITAMQVLAATLVGLQSVGLVVLVYGVVKKKKAANSAPALYAFAPAVVICW 75
 QY 79 VTMAYNNMSFGKELPIWGKAPALDOGLVGRALPATVHYRADSYEETAAVEELYPMAT 138
 DB 76 VLVGFRMAFGDRLLPFWMAKAGALTDPLVGRVAPVAPATAHSGSDGTLLETPTPEFYAEAA 135

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QY 139 VYFQCVFAAITLIVAGSLGRMSFLAMNIFVPLMLTSTYTGAFSLNGGFLFMGVY 198
DB 136 LVLFEPFPAITLIVLAGSLGRMNKAWMAFPPLMLTSTYTGAFSLNGGFLYOMGVY 195
QY 199 DYCGGVYIHVSAGIAGFTAAVWGPRAOXDRERFPNNIIFLTGTAGLMMGNAGNCGG 258
DB 196 DYSGGVYIHSSVAGFTAAVWGPRLKSDRERFSPNNILMAGGLMMGNAGNCGA 255
QY 259 PYANVSANAVLNTNICTAMSLIWTCLDVFIFPKKPSVVGAVQGNITGLVCTTPAAGV 318
DB 256 PYAPNVTATVAVLNTNVSATSLTMTCTDVFIFPKKPSVVGAVQGNITGLVCTTPAAGV 315
QY 319 OGMAALVGVLAGISIPYTMMLIHKRSKILQVDDTLGVHTHTGVAGLGLTGLPAEP 378
DB 316 HTWSAMLMGMFAGSVPMFTMMILHKKSTPLMKVDDTLAVFHTAVAGLGLVLTGLLAP 375
QY 379 TLGNLFLPVADSRGAFVGAAGAFGKQIAGLFFVAMNVVTSLICLAINTLVLPLMPD 438
DB 376 ELGALDCCPLPMMGVFY-GSGIGLGKQGLGALFVYVWMLVTSALLICGLFPLRMSD 434
QY 439 DKLEVGDAVHGEAYALMGDGMVDVTK 467
DB 435 DGLMGDDAHGEBAYALMGDGEKFDVTR 463

RESULT 11
AMT2 ARATH STANDARD; PRT; 475 AA.
ID AMT2 ARATH
AC 09M6N7;
DT 26-JUL-2002, integrated into UniProtKB/Swiss-Prot.
DT 24-MAY-2004, sequence version 2.
DT 07-MAR-2006, entry version 34.
DE Ammonium transporter 2 (ATAMT2).
GN Name:AMT2; Ordered locus names=at2g38290; ORF names=F16M14.22;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eucosids II; Brassicales; Brassicaceae; Arabidopsids.
OC NCBI_TaxID=3702;
RT [1]
RN NUCLEOTIDE SEQUENCE AND CHARACTERIZATION.
RP STRAIN=cv. C24; TISSUE=Root;
RC MEDLINE=20141244; PubMed=10675553; DOI=10.1016/S0014-5793(00)01153-4;
RA Sohlankamp C., Sheldon M.C., Howitt M.K.;
RA "Characterization of Arabidopsis ATAMT2, a novel ammonium transporter
in plants.";
RL FEBS Lett. 467:273-278 (2000).
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP STRAIN=cv. Columbia;
RC MEDLINE=20083487; PubMed=10617197; DOI=10.1038/45471;
RA Lin X., Kaul S., Rounsley S.D., Shree T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L.,
RA Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L.,
RA Taiton L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,
RA Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
RA Nieman W.C., White O., Eissen J.A., Salzberg S.L., Frazer C.M.,
RA Venter J.C.;
RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
thaliana.";
RL Nature 402:761-768 (1999).
CC -!- FUNCTION: Transports ammonium, probably in an energy-dependent
manner. Does not transport methylammonium.
CC -!- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein
(probable).
CC -!- TISSUE SPECIFICITY: Higher expression in shoots than roots.
CC -!- SIMILARITY: Belongs to the ammonium transporter (TC 2.A.49)
family.
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CC -----
DR EMBL: AF182039.1, AAP37192.1, -, mRNA.
DR EMBL: AC003028, AAM14857.1, -, Genomic DNA.
DR PIR: T01260, T01260.
DR GenomeReviews: CT485783_GR, AT2G38290.
DR GeneFarm: 3490, 317.
DR TAIR: At2g38290, -.
DR InterPro: IPR001905, Ammonium_transp.
DR InterPro: IPR010256, RH_like_transp.
DR InterPro: IPR002229, RheusRD.
DR PANTHER: PTHR11730, Ammonium_transp.1.
DR Pfam: PF00309, Ammonium_transp.1.
DR PRINTS: PR00342, RHESUSRD.
DR TIGRPFAM: TIGR00836, amt; 1.
DR PROSITE: PS01219, AMMONIUM_TRANSP, 1.
DR Ammonia_transport; Membrane; Polymorphism; Transmembrane; Transport.
KW CHAIN 1
FT FT 475
FT TRANSMEM 27 47
FT TRANSMEM 55 75
FT TRANSMEM 120 140
FT TRANSMEM 148 168
FT TRANSMEM 183 203
FT TRANSMEM 218 238
FT TRANSMEM 254 274
FT TRANSMEM 279 299
FT TRANSMEM 302 322
FT TRANSMEM 336 356
FT TRANSMEM 389 409
FT TRANSMEM 95 95
SQ SEQUENCE 475 AA; 50768 MW; A4958B0A8D2CAB60 CRC64;
Query Match 66.4%; Score 1682.5; DB 1; Length 475;
Best local Similarity 66.8%; Pred. No. 7.3e-116;
Matches 300; Conservative 61; Mismatches 77; Indels 11; Gaps 1;
QY 20 VADWLNKGNANOLVAATVIGLSVPGVLVVLGVGVKKKMAVNSAFMALYAPAAVVCWV 79
DB 12 VPEMLKGNANOLVAATVIGLSVPGVLVVLGVGVKKKMAVNSAFMALYAPAAVVCWV 71
QY 80 TWAYNMSFGEKLLPIWKKARPALDQGLVGRALPATVHYRADGSVETAAVEELYPMATV 139
DB 72 ILCTYKAFGEELLPIFGKGGKPAFDQGLYLGQAKIP-----NSNVAAHYPPMATL 120
QY 140 VYFQCVFAAITLIVAGSLGRMSFLAMNIFVPLMLTSTYTGAFSLNGGFLFMGVYD 199
DB 121 VYFQCVFAAITLIVAGSLGRMSFLAMNIFVPLMLTSTYTGAFSLNGGFLFMGVYD 180
QY 200 YCGGVYIHVSAGIAGFTAAVWGPRAOXDRERFPNNIIFLTGTAGLMMGNAGNCGG 259
DB 181 YSGGVYIHSSVAGFTAAVWGPRLKSDRERFSPNNILMAGGLMMGNAGNCGA 255
QY 260 PYANVSANAVLNTNICTAMSLIWTCLDVFIFPKKPSVVGAVQGNITGLVCTTPAAGV 319
DB 241 PYANVSANAVLNTNICTAMSLIWTCLDVFIFPKKPSVVGAVQGNITGLVCTTPAAGV 315
QY 320 GMAALVGVLAGISIPYTMMLIHKRSKILQVDDTLGVHTHTGVAGLGLTGLPAEP 379
DB 301 TWAALIIIGVSGTAPWASMIILHKKSALLQKDDTLAVFHTAVAGLGLVLTGLLAP 375
QY 380 LCNLFLPVADSRGAFVGAAGAFGKQIAGLFFVAMNVVTSLICLAINTLVLPLMPD 439
DB 361 LCVLVLPLPATRGAFFGSGKQLKQGLGALFVYVWMLVTSALLICGLFPLRMSD 434
QY 440 DKLEVGDAVHGEAYALMGDGMVDVTK 468
DB 421 ELGIDGDAHGEAYALMGDGEKFDVTR 463

RESULT 12
Q2QYV9 ORYSA PRELIMINARY; PRT; 458 AA.
ID Q2QYV9 ORYSA
AC Q2QYV9;

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DT 24-JAN-2006, integrated into UniProtKB/TrEMBL.
 DT 24-JAN-2006, sequence version 1.
 DT 07-FEB-2006, entry version 2.
 DE Ammonium transporter family.
 GN ORFNames=LOC_Os12g01420;
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae; BEP clade;
 OC Eriocaridaceae; Oryzaceae; Oryza.
 NCBI_TaxID=39947;
 RN (1)
 RP NUCLEOTIDE SEQUENCE.
 RA Buehl C.R., Wing R.A., McCombie W.A., Ouyang S.;
 RL Submitted (Apr-2005) to the EMBL/GenBank/DBJ databases.
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 CC -----
 DR EMBL: DP000011; ABA95601.1; -; Genomic DNA.
 DR SQA SEQUENCE 458 AA; 48077 MW; 3B2CAC65204BF2A CRC64;
 Query Match 56.7%; Score 1436; DB 2; Length 458;
 Best Local Similarity 59.4%; Pred. No. 1.1e-97;
 Matches 262; Conservative 73; Mismatches 98; Indels 8; Gaps 3;
 QY 17 SASVADMLKGNAMQVLAATLVGLQSVGLVLYGVGVKKKMAVNSAFMALYAFAAVMI 76
 DB 3 SVAVEPMILKGNAMQVLAATLVGLQSVGLVLYGVGVKKKMAVNSAFMALYAFAAVMI 62
 QY 77 CWVTAANNYSFSEKLLPIWGKARPALDQGLVGRALPATVHYRADSVETAAVEELPM 136
 DB 63 CALMAHNNAFVGHRLPFGVGRAPALAQHYMLTQALLPFTLHLSNGEVETAAVAPLYPS 122
 QY 137 AVVVYFQCPAATLTLIVAGSLGRMSFLAMMIFVPLMLTFSTYVAFSLMGSGFLFHNG 196
 DB 123 ASMVEFQMASAGVTGLVAGAVLGRMSVAKMAFVPLMTLSTVGAYSIWGGFLFHNG 182
 QY 197 VIDYCGGVYIHVSAGIAGFTAAVYVGPRAOKDERPP--NNILFTLTAGLLMGMAGFN 254
 DB 183 VMDYSGGVYVHLAAGVSGTAAVYVGPRAKEBEEMTAGGNNLVANVAGLLMGMAGFN 242
 QY 255 NGGQPVANSVSAVAVLNTNICTAMSLIWTCLDVIFFKPSVGAAGMIGLVCITPA 314
 DB 243 NGGDPFSANTDSVAVLNTNICTTTSILAMVCCDIAGRPSVGAAGMIGLVCITPA 302
 QY 315 AGVVGMAALWGVLAGSIPWYTMMLHRSKTLQVDDTLGVFHTHGVAGLLGLTGL 374
 DB 303 AGLVQGMALWGVLAGSIPWYTMMLHRSKTLQVDDTLGVFHTHGVAGLLGLTGL 357
 QY 375 AEPPTCNLFPLPADRGAFFYG-GAGGAQFGKIAGGLFVAVANNVVTSLICLAINLLVPLR 433
 DB 358 FAHPFTLCMFLPFTGSRGLVYGRAGGVYLVKVAALFVAAVNVAAITSLIVVVAAPFP 417
 QY 434 LAMPDDKLEVGDDAVHGEAVY 454
 DB 418 LMTTEDELLAGDIAVHGEQAY 438
 RESULT 13
 Q3EBK4 ARATH PRELIMINARY; PRT; 359 AA.
 AC Q3EBK4;
 DT 08-NOV-2005, integrated into UniProtKB/TrEMBL.
 DT 07-FEB-2006, entry version 4.
 DE Protein At2g38290.
 GN OrderedLocustNames=At2g38290;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliopsida; eudicotyledons; core eudicotyledons;
 OC Rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 NCBI_TaxID=3702;
 RN (1)

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=cv. Columbia;
 RX MEDLINE=20083487; PubMed=10617197; DOI=10.1038/45471;
 RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
 RA Fujii C.Y., Mason T.M., Bowman C.U., Barneshead M.E., Feldblyum T.V.,
 RA Buehl C.R., Ketchum K.A., Lee J.D., Ronning C.M., Koo H.U.,
 RA Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L.,
 RA Tallon L.J., Gill J.B., Adams M.D., Carrera A.J., Creasy T.H.,
 RA Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
 RA Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
 RA Venter J.C.;
 RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
 thaliana."
 RL Nature 402:761-768 (1999).
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 CC -----
 DR TAIR; At2g38290; -;
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0008519; F:ammonium transporter activity; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR001905; Ammonium_transp.
 DR InterPro; IPR010256; R:like_transp.
 DR Pfam; PF00909; Ammonium_transp; 1.
 DR PRINTS; PR00342; RHESUSRD.
 DR PROSITE; PS01219; AMMONIUM_TRANSNP; UNKNOWN 1.
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 Query Match 51.2%; Score 1297; DB 2; Length 359;
 Best Local Similarity 68.5%; Pred. No. 1.7e-87;
 Matches 228; Conservative 50; Mismatches 55; Indels 0; Gaps 0;
 QY 136 MATVYFQCPAATLTLIVAGSLGRMSFLAMMIFVPLMLTFSTYVAFSLMGSGFLFHNM 195
 DB 1 MATVYFQCPAATLTLIVAGSLGRMSFLAMMIFVPLMLTFSTYVAFSLMGSGFLFHNM 60
 QY 196 GVIDYCGGVYIHVSAGIAGFTAAVYVGPRAOKDERPPNNILFTLTAGLLMGMAGFN 255
 DB 61 GVIDYSGGVYVHLAAGVSGTAAVYVGPRAKDERPPNNVLMALAGLLMGMAGFN 120
 QY 256 GGGQPVANSVSAVAVLNTNICTAMSLIWTCLDVIFFKPSVGAAGMIGLVCITPA 315
 DB 121 GGAPVAAVNTSIVLNTNLSAATSLIWTCLDVIFFKPSVGAAGMIGLVCITPA 180
 QY 316 GVVQGMALWGVLAGSIPWYTMMLHRSKTLQVDDTLGVFHTHGVAGLLGLTGL 375
 DB 181 GLIQTMAAIIIGVSGTAPWASMTIHKRSALQVDDTLGVFHTHGVAGLLGLTGL 240
 QY 376 AEPPTCNLFPLPADRGAFFYG-GAGGAQFGKIAGGLFVAVANNVVTSLICLAINLLVPLR 435
 DB 241 AHPDLCVLTPLPATRGAFFYGNGSKQLLKQLAGAFAVANNVVTSLIILAIRVFIPLR 300
 QY 436 MPDDKLEVGDDAVHGEAVYALMGDEMYDVTKH 468
 DB 301 MAEEELIGIDDAHGEAVYALMGDEKEDPATRH 333
 RESULT 14
 Q2RBN4 ORYSA PRELIMINARY; PRT; 326 AA.
 AC Q2RBN4;
 DT 24-JAN-2006, integrated into UniProtKB/TrEMBL.
 DT 07-FEB-2006, entry version 1.
 DE Ammonium transporter AMT2.1, putative.
 GN ORFNames=LOC_Os11g01410;
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae; BEP clade;
 OC Eriocaridaceae; Oryzaceae; Oryza.
 NCBI_TaxID=39947;

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RN      [1]
RP      NUCLEOTIDE SEQUENCE.
RA      Buell C.R., Wing R.A., McCombie W.A., Ouyang S.,
RL      Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
CC      -----
CC      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
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CC      -----
DR      EMBL: DP000010; AB91064.1; -; Genomic DNA.
SQ      SEQUENCE 326 AA; 34717 MW; D106D9F1A38C91D3 CRC64;

Query Match      40.6%; Score 1030; DB 2; Length 326;
Best Local Similarity 58.3%; Pred. No. 7.9e-68;
Matches 183; Conservative 56; Mismatches 71; Indels 4; Gaps 1;

QY      17 SASVADMLNKGDNAWLVLAATLVGLQSVPLVLYGGVKKKVAVNSAFMALYAFRAVMI 76
      ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      3 SAAVPEMLNKGDNAKMLSTLVLAQGFPLALFYGVAPRKVALTSAFVALYAMATMP 62
      ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      77 CWTWAVNNSFGEKLPYWGKARPALDQGLVGRPALPATVHYRADGSVETAAVEPLYPM 136
      ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      63 CMALMAHNAHNAFGRRLLPFVGRPAALADYMLSQLLPSTLHRSNGEVETAAVADLPYS 122
      ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      137 AATVYVCVPAATLTLIVAGSLIGRMSFLAMMI FVPLMTFSYTVGAFSLMGGLFHHG 196
      ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      123 ASNVFFQWAPAGVTVGLVAGAVLGRMSVKAMMAFVPLMTLSTYVGAVSLMGGLFHHG 182
      ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      197 VIVYCGGYVIVHAGIAGFTAAVWVGPRADKRRER---FPNNILFTLTGAGILMWGVA 252
      ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      183 VMDYSGYVLLAAGVSGYTRATWVGPRKREDEEMATSGNLVVMVAGAILMMGMT 242
      ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      253 GENGSGPYAANSVASNAVLNTNICTAMSLIVTCLDVIFFPKPSVYGVANQGITGLVCTT 312
      ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      243 GFEGGDPFSANTDSVAIVNTHTICATTSIVAMVCCVAVAGRPSVVGAVGMITGLVCTT 302
      ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      313 PAAGVVGMAALVM 326
      ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      303 PRSNIRYSFLVLVI 316
      ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 15
Q974J8 SULTO PRELIMINARY; PRT; 518 AA.
AC      Q974J8;
DT      01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT      01-DEC-2001, sequence version 1.
DT      07-FEB-2006, entry version 17.
DE      S18aa long hypothetical ammonium transporter.
GN      OrderedLocustNames=ST0661;
OS      Sulfolobus tokodaii.
OC      Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC      Sulfolobus.
OX      NCBI_TaxID=111955;
RA      NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP      STRAIN=OCM 10545 / 7;
RC      MEDLINE=21456156; PubMed=11572479; DOI=10.1093/dnares/8.4.123;
RA      Sekine M., Baba S., Aikai A., Koenig H., Hosoyama A., Fukui S.,
RA      Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,
RA      Yoshizawa T., Tanaka T., Kudo Y., Yamazaki J., Kushida N., Oguchi A.,
RA      Aoki K., Maeda S., Yanagii M., Nishimura M., Yamagishi A., Oshima T.,
RA      Kikuchi H.;
RT      "Complete genome sequence of an aerobic thermophilic
RT      Crenarchaeon, Sulfolobus tokodaii strain7.";
RL      DNA Rep. 8:123-140(2001).
CC      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
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CC      -----
EMBL: BA000023; BAB5560.1; -; Genomic DNA.
DR      BioCyc; STOK111955:ST0661-MONOMER; -.
DR      GO; GO:0016020; C:membrane; IEA.

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DR      GO; GO:008519; F:ammonium transporter activity; IEA.
DR      GO; GO:006810; P:transport; IEA.
DR      InterPro; IPR001905; Ammonium_transpt.
DR      InterPro; IPR010256; Rh_like_transpt.
DR      InterPro; IPR002229; RheusRHD.
DR      PANTHER; PTHR11730; Ammonium_transpt; 1.
DR      Pfam; PF00909; Ammonium_transp; 1.
DR      PRINTS; PR00342; RHEUSRHD.
DR      TIGRFAMs; TIGR00836; amc; 1.
DR      PROSITE; PS01219; AMMONIUM_TRANS_P.
KW      Complete proteome; Hypothetical protein.
SQ      SEQUENCE 518 AA; 55179 MW; 990E469463D68DBD CRC64;

Query Match      40.4%; Score 1023.5; DB 2; Length 518;
Best Local Similarity 47.9%; Pred. No. 3.8e-67;
Matches 217; Conservative 66; Mismatches 145; Indels 25; Gaps 10;

QY      10 LAYQNT---SASVADMLNKGDNAWLVLAATLVGLQSVPLVLYGGVKKKVAVNSAF 65
      ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      51 LALEHTADYPSAAVSWLDTGSMNMLTRATFVGLQSVGVALLYAGLSKKKVAVNSAL 110
      ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      66 MALYAPAAVVICWTVWAVNNSFGE-KLPIWGKARPALDQGLVGRPALPATV-HYRADG 123
      ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      111 MVFYAPAAVIVVMVMIAGVNAFGHPALLSING-----YGIL--GYPLPAMLGHYEASQ 161
      ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      124 SVETAAVEPL-YPMATVYVFCQVFAITLIVAGSLIGRMSFLAMMIFVPLMTFSYTVG 182
      ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      162 TVFGPTGTVDIPTSTYIFQVFAITVLLAGVLEHKNFAMMI FVPFNSLVISPV 221
      ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      183 AFSLMGSGFLFHHGVLDYCGYVIVHAGIAGFTAAVWVGPRADKRRERFPNNILFTLT 242
      ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      222 AYVLPFGGMLNQLGAVDFSGGYIIVHDAGVLAALAAIGPLASLR-KLEAHSLLVLA 280
      ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      243 GAGILMWGNAFNGGPGPYAANSVASNAVLNTNICTAMSLIVTCLDVIFFPKPSVYGA 302
      ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      281 GAGILMWGMDGFNGGDPGATIDAAIAIVNTNATVSAITWMLMDMAFFKKPTLVGATS 340
      ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      303 GMTGLVCTTPAAGVVGMAALVMGVLASIPYTMILHKSILIORVDDTLGVFHTG 362
      ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      341 GAITGLVAITPPAAGVNGWEAMLIIGASISIPWLSYKKEPRLK---VDDTLGVFHTG 396
      ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      363 VAGLIGGLLTGLFAEPTLGNLFLPVADSRGAFFYGAGAGQFGKQIAGGLFVVAANVVT 422
      ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      397 IAGIVGGLTGVADPNVQYVDPFL--KGLYGNL--YQLGQAAAANVVFYDPAIRF 452
      ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      423 LICTAINTLVPLMPDDKLEVGDDAVHGEAAY 455
      ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      453 GILKILGLFIPLOAPPDTLAIGDYAMHGEVAYS 485
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Search completed: July 22, 2006, 03:32:58
 Job time : 304 secs

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OM protein - protein search, using sw model

Run on: July 22, 2006, 03:33:11 ; Search time 50 Seconds
(without alignment)
838,543 Million cell updates/sec

Title: US-10-713-648a-63
Perfect score: 2534
Sequence: 1 MESSATVPLAQCNTSASV.....GEMVDTKKGDAAPVIV 479

Scoring table: BLOSUM62
Gapop 10.0 , Gapept 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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3: /EMC_Celerra_SIDS3/prodata/2/1aa/7-COMB.pep:*
4: /EMC_Celerra_SIDS3/prodata/2/1aa/H-COMB.pep:*
5: /EMC_Celerra_SIDS3/prodata/2/1aa/PCTUS-COMB.pep:*
6: /EMC_Celerra_SIDS3/prodata/2/1aa/RB-COMB.pep:*
7: /EMC_Celerra_SIDS3/prodata/2/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2216	87.5	470	US-10-033-109-14	Sequence 14, Appl
2	1860.5	73.4	486	US-10-033-109-12	Sequence 12, Appl
3	1715.5	67.7	497	US-10-033-109-10	Sequence 10, Appl
4	717.5	28.3	455	US-09-252-991A-23745	Sequence 23745, A
5	641	25.3	439	US-09-489-039A-12960	Sequence 12960, A
6	639	25.2	433	US-09-543-681A-6105	Sequence 6105, Ap
7	634.5	25.0	470	US-09-328-352-5397	Sequence 5397, Ap
8	582	23.0	437	US-09-134-001C-3907	Sequence 3907, Ap
9	532	21.0	463	US-09-902-540-15324	Sequence 15324, A
10	506	20.0	499	US-09-487-558B-194	Sequence 194, App
11	476	18.8	452	US-09-602-787A-398	Sequence 398, App
12	474.5	18.7	492	US-09-487-558B-192	Sequence 192, App
13	338.5	13.4	501	US-08-635-967-2	Sequence 2, Appl1
14	335	13.2	361	US-09-134-000C-5907	Sequence 5907, Ap
15	313.5	12.4	500	US-10-033-109-4	Sequence 4, Appl1
16	305	12.0	494	US-10-033-109-6	Sequence 6, Appl1
17	284	11.2	63	US-10-033-109-8	Sequence 8, Appl1
18	275	10.9	441	US-09-328-352-4217	Sequence 4217, Ap
19	260.5	10.3	464	US-09-252-991A-18525	Sequence 18525, A
20	244	9.6	175	US-09-248-796A-20751	Sequence 20751, A
21	233.5	9.2	223	US-09-107-532A-3674	Sequence 3674, Ap
22	232	9.2	185	US-09-602-787A-2	Sequence 2, Appl1
23	214	8.4	224	US-09-107-532A-10193	Sequence 4102, Ap
24	208	8.2	240	US-09-248-796A-20193	Sequence 20193, A
25	178.5	7.0	487	US-09-949-016-9649	Sequence 9649, Ap
26	176.5	7.0	418	US-09-949-016-7328	Sequence 7328, Ap

27	129	5.1	607	2	US-09-252-991A-26825	Sequence 26825, A
28	128.5	5.1	470	2	US-09-603-208A-246	Sequence 246, App
29	128	5.1	183	2	US-10-033-109-2	Sequence 2, Appl1
30	124	4.9	303	2	US-09-372-934-2	Sequence 2, Appl1
31	124	4.9	303	2	US-09-766-916-2	Sequence 2, Appl1
32	124	4.9	303	2	US-09-766-898-2	Sequence 2, Appl1
33	124	4.9	303	2	US-09-637-040C-2	Sequence 2, Appl1
34	124	4.9	303	2	US-10-306-249-2	Sequence 2, Appl1
35	124	4.9	303	3	US-10-306-247-2	Sequence 2, Appl1
36	122	4.8	886	2	US-09-902-540-11981	Sequence 11981, A
37	119.5	4.7	458	2	US-09-252-991A-27645	Sequence 27645, A
38	118	4.7	413	2	US-09-543-681A-5108	Sequence 5108, Ap
39	118	4.7	321	2	US-09-252-991A-31084	Sequence 31084, A
40	117.5	4.6	91	2	US-09-602-787A-4	Sequence 4, Appl1
41	116.5	4.6	315	2	US-09-252-991A-28791	Sequence 28791, A
42	116	4.6	548	2	US-09-328-352-6605	Sequence 6605, Ap
43	114.5	4.5	457	2	US-09-902-540-15123	Sequence 15123, A
44	114.5	4.5	509	2	US-09-252-991A-24098	Sequence 24098, A
45	112.5	4.4	382	2	US-09-902-540-10508	Sequence 10508, A

ALIGNMENTS

RESULT 1
US-10-033-109-14
Sequence 14, Application US/10033109
Patent No. 6833492
GENERAL INFORMATION:
APPLICANT: Allen, Stephen M.
APPLICANT: Rafaleki, J. Antoni
TITLE OF INVENTION: Nitrogen Transport Metabolism
FILE REFERENCE: BB-1210
CURRENT APPLICATION NUMBER: US/10/033,109
CURRENT FILING DATE: 2001-12-28
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/384,625
PRIOR FILING DATE: EARLIER FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/098,248
PRIOR FILING DATE: EARLIER FILING DATE: 28 August 1998
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Microsoft Office 97
SEQ ID NO 14
LENGTH: 470
TYPE: PRT
ORGANISM: Trilicium aestivum
US-10-033-109-14
Query Match 87.5%; Score 2216; DB 2; Length 470;
Best Local Similarity 86.0%; Pred. No. 5.7e-213;
Matches 404; Conservative 30; Mismatches 34; Indels 2; Gaps 1;
QY 8 VPLAYGNTSASVADMLNKGNAMQVLAATLVGLQSVPLVVLVYGVVKKKMAVNSAFMA 67
3 VPVAYGNTSASVADMLNKGNAMQVLAATLVGLQSVPLVVLVYGVVKKKMAVNSAFMA 62
QY 68 LVAFAAVICWTWAVNMSFGEKLEPIKWKARPALDQGLVGRALPATVHYADDSVET 127
63 LVAFAAVICWTWAVNMSFGEKLEPIKWKARPALDQGLVGRALPATVHYADDSVET 122
QY 128 AAVEPYPMAVTVVPCVFAATLILVAGSLGRMSFLAMNIPVPLMFLPSYVGAFLSW 187
123 AAVEPYPMAVTVVPCVFAATLILVAGSLGRMSFLAMNIPVPLMFLPSYVGAFLSW 182
QY 188 GGGFLFMWGVIDCGGVVHVSAGIAGFTAAVWVGRPAOKDRRFPNNILFTLTGAGLL 247
183 GGGFLFMWGVIDCGGVVHVSAGIAGFTAAVWVGRPAOKDRRFPNNILFTLTGAGLL 242
QY 248 WKGWAGPFGGPPYAAVNSVAMAVLNTNICTANSLIYWTCLDVIFFKKPSVGAVOGMITG 307
243 WKGWAGPFGGPPYAAVNSVAMAVLNTNICTANSLIYWTCLDVIFFKKPSVGAVOGMITG 302
QY 308 LVCTITPAAGVVGWMAVWGVLAGSLPWTYTMILHKRSKILQVRDVLGVFHTHGVAGLL 367

Db 303 LVCITPGAGVCGMAGLWGLVAGSVPMYTMVILHRSKSLDRVDDTLCVITHGVAGLL 362
Qy 368 GGLTGLFAEPPTLCNLFLPVADSRGAFYGGAGGAGFGKQIAGLGFVVMNVVTSLICLA 427
Db 363 GGLTGLFAEPPTLCNLFLPVADSRGAFYGGAGGAGFGKQIAGLGFVVMNVVTSLICLA 422
Qy 428 INLVPLMPDCKLEVGDAVHGEERYALMGCEMYDTYKHSDDAAVAVP 477
Db 423 IRLVPLRSEKELAIIGDDAVHGEERYALMGCEMYDTYKHSDDAAVAVP 470

RESULT 2

US-10-033-109-12
Sequence 12, Application US/10033109
Patent No. 6833492
GENERAL INFORMATION:
APPLICANT: Allen, Stephen M.
APPLICANT: Rafalski, J. Antoni
APPLICANT: Sakai, Hajime
TITLE OF INVENTION: Nitrogen Transport Metabolism
FILE REFERENCE: BB-1210
CURRENT APPLICATION NUMBER: US/10/033,109
CURRENT FILING DATE: 2001-12-28
PRIOR FILING DATE: EARLIER APPLICATION NUMBER: 09/384,625
PRIOR FILING DATE: EARLIER FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/098,248
PRIOR FILING DATE: EARLIER FILING DATE: 28 August 1998
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Microsoft Office 97
SEQ ID NO 12
LENGTH: 486
TYPE: PRT
ORGANISM: Glycine max
US-10-033-109-12

Query Match 73.4%; Score 1860.5; DB 2; Length 486;
Best Local Similarity 71.9%; Pred. No. 2,2e-177;
Matches 341; Conservative 51; Mismatches 77; Indels 5; Gaps 2;

Qy 9 PLAYOGNTSASVADWLNKGDNAQVLAATLVGLQSVGLVLYGGVKKKMAVNSAFML 68
Db 4 PLAYOGNTSASVADWLNKGDNAQVLAATLVGLQSVGLVLYGGVKKKMAVNSAFML 62
Qy 69 YAFPAVWICWVWYVYMAFGEBELFPWVGAPALGQKFLTKRAIVETIHFNDNGVESP 128
Db 63 YAFPAVWICWVWYVYMAFGEBELFPWVGAPALGQKFLTKRAIVETIHFNDNGVESP 122
Qy 129 AVEPLYPMAVTVYFQCVFAITLILVAGSLGMSFLAMMIFVPLWLTFSYVGAFFSLWG 188
Db 123 PEEPTYPMAVTVYFQCVFAITLILVAGSLGMSFLAMMIFVPLWLTFSYVGAFFSLWG 182
Qy 189 GGFLEHMGVIDYCGGYVIVHSAGIAGFTAAVYVGPRAQKDEREPNNILFTLTGAGLLM 248
Db 183 GGFLEHMGVIDYCGGYVIVHSAGIAGFTAAVYVGPRAQKDEREPNNILFTLTGAGLLM 242
Qy 249 MCMWAGNNGGEPYANASVASMALVNTMTCTAMSLIWTCLDVIFFKKPSVYVGAQGITEL 308
Db 243 MCMWAGNNGGEPYANASVASMALVNTMTCTAMSLIWTCLDVIFFKKPSVYVGAQGITEL 302
Qy 309 VCITPAAGVVGMAALVWGLVAGSIPWYTMVILHRSKSLDRVDDTLCVITHGVAGLLG 368
Db 303 VCITPAAGVVGMAALVWGLVAGSIPWYTMVILHRSKSLDRVDDTLCVITHGVAGLLG 362
Qy 369 GGLTGLFAEPPTLCNLFLPVADSRGAFYGGAGGAGFGKQIAGLGFVVMNVVTSLICLA 428
Db 363 GGLTGLFAEPPTLCNLFLPVADSRGAFYGGAGGAGFGKQIAGLGFVVMNVVTSLICLA 422
Qy 429 INLVPLMPDCKLEVGDAVHGEERYALMGCEMYDTYKHSDDAAVAVP 478
Db 423 IRLVPLRSEKELAIIGDDAVHGEERYALMGCEMYDTYKHSDDAAVAVP 476

RESULT 3
US-10-033-109-10
Sequence 10, Application US/10033109
Patent No. 6833492
GENERAL INFORMATION:
APPLICANT: Allen, Stephen M.
APPLICANT: Rafalski, J. Antoni
APPLICANT: Sakai, Hajime
TITLE OF INVENTION: Nitrogen Transport Metabolism
FILE REFERENCE: BB-1210
CURRENT APPLICATION NUMBER: US/10/033,109
CURRENT FILING DATE: 2001-12-28
PRIOR FILING DATE: EARLIER APPLICATION NUMBER: 09/384,625
PRIOR FILING DATE: EARLIER FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/098,248
PRIOR FILING DATE: EARLIER FILING DATE: 28 August 1998
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Microsoft Office 97
SEQ ID NO 10
LENGTH: 497
TYPE: PRT
ORGANISM: Oryza sativa
US-10-033-109-10

Query Match 67.7%; Score 1715.5; DB 2; Length 497;
Best Local Similarity 69.3%; Pred. No. 7.4e-163;
Matches 312; Conservative 54; Mismatches 83; Indels 1; Gaps 1;

Qy 19 SVADMINKGDNAQVLAATLVGLQSVGLVLYGGVKKKMAVNSAFMALYAFPAVWICW 78
Db 16 AVEPLYPMAVTVYFQCVFAITLILVAGSLGMSFLAMMIFVPLWLTFSYVGAFFSLWG 75
Qy 79 YAFPAVWICWVWYVYMAFGEBELFPWVGAPALGQKFLTKRAIVETIHFNDNGVESP 138
Db 76 YAFPAVWICWVWYVYMAFGEBELFPWVGAPALGQKFLTKRAIVETIHFNDNGVESP 135
Qy 139 VYFQCVFAITLILVAGSLGMSFLAMMIFVPLWLTFSYVGAFFSLWG 198
Db 136 VYFQCVFAITLILVAGSLGMSFLAMMIFVPLWLTFSYVGAFFSLWG 195
Qy 199 DYCGGYVIVHSAGIAGFTAAVYVGPRAQKDEREPNNILFTLTGAGLLM 258
Db 196 DYCGGYVIVHSAGIAGFTAAVYVGPRAQKDEREPNNILFTLTGAGLLM 255
Qy 259 PYANASVASMALVNTMTCTAMSLIWTCLDVIFFKKPSVYVGAQGITEL 318
Db 256 PYANASVASMALVNTMTCTAMSLIWTCLDVIFFKKPSVYVGAQGITEL 315
Qy 319 GGMALVWGLVAGSIPWYTMVILHRSKSLDRVDDTLCVITHGVAGLLG 378
Db 316 GGMALVWGLVAGSIPWYTMVILHRSKSLDRVDDTLCVITHGVAGLLG 375
Qy 379 TLCLFLPVADSRGAFYGGAGGAGFGKQIAGLGFVVMNVVTSLICLA 438
Db 376 TLCLFLPVADSRGAFYGGAGGAGFGKQIAGLGFVVMNVVTSLICLA 434
Qy 439 DKLGVGDDAVHGEERYALMGCEMYDTYKHSDDAAVAVP 468
Db 435 DKLGVGDDAVHGEERYALMGCEMYDTYKHSDDAAVAVP 464

RESULT 4
US-09-252-991A-23745
Sequence 23745, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107136.136
CURRENT FILING DATE: US/09/252,991A
PRIOR APPLICATION NUMBER: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788

Query Match	25.3%	Score 641;	DB 2;	Length 439;
Best Local Similarity	33.6%;	Pred. No. 2e-55;		
Matches 149;	Conservative	78;	Mismatches 167;	Indels 50;
				Gaps 8
QY	19	SVADMLNGGDNAWQVLAATLVGLGSGVPGELVVTYGGVKKKRAVNSAFMLALYFAAIVICW	78	

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QY      2  LKNGDANMOUVAATLVGLQDSVGLVTVLGGVYKKCKWAANSFMAHYEFAAWICWYMAW  83
Db      31  IDKADNSFMILICALVFMFTITPGIALFYGGILSRKSNVSLMTQWMLFVSVIIIMINFG  90
QY      84  NMSF--GEKLLPTWKGARPALDQGLLVGRBALPATVHRADGSVEITAVELEYMATVY  144
Db      91  SLAFTAGNK---TWG-----GMSLTENNISDVSAVG--INQYHV  128
QY      142  FOCFPAITLLIVAGSLIGRMSFLAMMIFVPLMLTFSYTVGAFLSQ--GGEFLFMGVIDY  200
Db      129  FQSPFAITVALLVGLGERIFPSALLFETVIMPFPSYIPAHHWGCGGWLIDDGALDF  188
QY      201  CGGVTVHVSAGTGFPAATWNGBPQOKRERPEPNLILFTLLTGALLMAGAGFNCGAPY  260
Db      189  AGGTVHINNAVALVGAITLGRKEDYCHTAKPNIENMVTGTNAVLYIGMFGFNASAG  248
QY      261  AANSVAMAVLNTNICTAMSLVWTCLDVITFPKRSVVGAVQGMITGLVCTTPAAGYOG  320

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Db 249 SANGIALALFLNTVATAGAVLAWTFAEWLVRKPSMLGSGSCGCIAGLVAITPAAGTVGP 308
Qy 321 WAALVAGVLAGISIPYTMMLHKRSKILORVDDTLGVFHTHVAGLGLTGLFAEPFL 380
Db 309 IGAIVGIIAGIIGMGVVLKRWMLK---ADVDVDFVGHGTCTIAGLGLTGIPT--- 360
Qy 381 CNLFLPVADSRGAFYGGAGGAG---FGKOIAGLGFVVA---MNVTVTSICLAINLLVP 433
Db 361 -----ASFVGGICYSCHMTLKGKOVLTQLPSVVTLLIWSVVAIARIKADKLVG 409
Qy 434 LAMPDDKLEVG-DDAVHGEAY 454
Db 410 LRVSGEEHHDGLDITTHGERAY 431

RESULT 7
US-09-328-352-5397
; Sequence 5397, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5397
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5397

Query Match 25.0%; Score 634.5; DB 2; Length 470;
Best Local Similarity 32.5%; Pred. No. 1e-54;
Matches 150; Conservative 82; Mismatches 176; Indels 53; Gaps 8;

Qy 3 SATATVPLAYQGNSTSVADMINKGDMQVLAATLVGLQSVPGVLVLYGVYKKKMAVN 62
Db 48 ATIAAPAAEETPAATPTAKLDGTGTSMILSTALVLTMTIPGLAFYGMVRKKXNVLS 107
Qy 63 SAFMALYAPAAVMIQVNTVAVNMSEFGEKLLPIWGKARPALDQGLVGRA--ALPATVHYR 120
Db 108 TMMPFSLSAIIVSLMVLINGYSIAFSGT-----GAFGDLSKAMLVAFDALSGTI--- 159
Qy 121 ADGSVETAVERLYPMATVTVVFCVFAATLLIVAGSLIGRMSFLAMMIFVPLMLTFESTY 180
Db 160 -----PESLFIIFQMTFAITVAIILSGSIADRMKYSAFMAFIAMVLVVA 205
Qy 181 VGAFSLWGG-GFLFMHGVLDYCGGYIHYISAGIAGTAAYWGPRAQKDBRFRPPNLIIF 239
Db 206 PTHHWVMAADGMLEFKAGLDPAFGTVIHNSGVAGLVAAVMDGKRGICLRESMAFNLLTL 265
Qy 240 TLTGAGLIMMGWAGFGGPPYAAVNSAVSMAVNTNICTAMSLIWTCLDVIFFKPSVVG 299
Db 266 TVIGASLIMVGMFGFSGSALGAGASVAILVTQVAAAALAAAFSMILVERMTRGASVVG 325
Qy 300 AVQGMITGLVCTTPAAGVVGMAALVMGVLAGISIPYTMMLHKRSKIIQVDDTLGVFH 359
Db 326 GASGAVAGLVITTPAAGFVGAGALVMGLIGVAVCFWGITAL---KRLIKADDAIDAFG 381
Qy 360 THGVNGLGLLTGLF-----AEPFLCNLFLPVADSRGAFYGGAGAGGAGKQIAGL 411
Db 382 LHAVGGIVGAILGVVYSDEITIAKANAVLAPTF-----AGQLWVQEGVL 426
Qy 412 PVVAMNVVTSLSICLAINLLVPLRMPDDKLEVG-DDAVHGE 451
Db 427 AMVYVSGIATFILLKYIDILIGLRVNSDDERMGLDLSQGE 467

RESULT 8
US-09-134-001C-3907
; Sequence 3907, Application US/09134001C
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; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 3907
; LENGTH: 437
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3907

Query Match 23.0%; Score 582; DB 2; Length 437;
Best Local Similarity 29.7%; Pred. No. 1.6e-49;
Matches 136; Conservative 93; Mismatches 171; Indels 58; Gaps 11;

Qy 24 INKGDNAQLVAATLVGLQSVPGVLVLYGVYKKKMAVNSAFMALYAPAAVMIQVNTWAY 83
Db 22 MNMDITFLPCTLLVLMNT-PGLSLFYGLVQSKNALNTWQSNVAIVTFVWIIIGF 80
Qy 84 NMSF-----GKTLPIWGKARPALDQGLVGRBALPATVHYRAQSVETAVERLYP 135
Db 81 SLSPDGNQWIGKFL-----GL-----HH--VGFTSKTSLPHIP 115
Qy 136 MATVYFQCVPAATLLIVAGSLGRMSFLAMMIFVPLMTFSYTVGAFSLMGGFLEPHW 195
Db 116 LSLFMLPQMFCTIAVSLSSIAEKRFIYLLFVSLMVLIIISPAVHWVWGGWISKI 175
Qy 196 GVIDYCGYVIVHVSAGIAGFTAAVWGPRAQKDBRFRPPNLIPTLTGAGLLMGWAGFN 255
Db 176 GAIIDVAGGTVVHTSGVGLVIGMIG--IGKKKEKHPHMLITLLIGLILVLMGWYFN 233
Qy 256 GGGPAAVNSVSMVAVLNTNICTAMSLIWTCLDVIFFKPSVGVAGVQGMITGLVCTPAA 315
Db 234 VGSATPFHAMISFVNVIASAGAFGMLIFEYILKKTSLTGLIGLSGLVAITPAA 293
Qy 316 GVVQGMALMVGVLGSIIPYTMMLHKRSKILORVDDTLGVFHTHVAGLGLTGLF 375
Db 294 GYVSTMSMTIAIIGICICIVINLI---KVKQYNDALDAFGHGGILGAVLTGVF 349
Qy 376 ----AEPFLCNLFLPVADSRGAFYGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 431
Db 350 QSHQNSAVQNGFIYADFKVVI-----QLGAALIVVPSAIVTFELIARFIKIF 399
Qy 432 VPLRMPDDKLEVGDDA-VHGEBAVYLMGDGEMVDTYTKH 468
Db 400 TPLATTOEDKGTGLDAIVHGEKAYFY---GELINKENRH 434

RESULT 9
US-09-902-540-15324
; Sequence 15324, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Steven C.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 15324
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; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932180.9
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932182.5
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932190.6
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932191.4
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932209.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932212.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932227.9
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932228.7
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932229.5
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932230.9
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932927.3
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19933005.0
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19933006.9
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19940764.9
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19940765.7
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19940766.5
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19940830.0
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19940831.9
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19940832.7
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19940833.5
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19941378.9
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: DE 19941379.7
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: DE 19941395.9
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: DE 19942077.7
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: DE 19942078.5
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: DE 19942079.3
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: DE 19942088.2
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 678
; SEQ ID NO 398
; LENGTH: 452
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
; US-09-602-787A-398

Query Match      18.8%; Score 476; DB 2; Length 452;
Best Local Similarity 30.2%; Pred. No. 6.8e-39;
Matches 139; Conservative 70; Mismatches 180; Indels 72; Gaps 13;

24 LKNGNAMOVLVATVGLVSVGLVVLVYGVVKKKVAVSAPFAVAFVAVICWTVAY 83
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1 MPPSLWALIAFALVSLM-FRELSTLYGGMGCGHVLTFFMVMVSSLGIIISVYIYGH 59
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

84 NNSFSEKL-----LPIWGKARPALDOGLLVGRALPATVHYRADSGSVETAVERPLY 134
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 60 GLVLGNSIGGWGIGNPLEYFGFRNIMEDG-----TQDLMMAG----- 98
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135 PMATVVYQCVFAATILLVAGSLIGRMSFLAMMI FVPLMLTFSTYVCAF-----S 185
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 99 -----FYILFAAISLALVSSGAAGRPFAMLVPGVLMFTFYAPLAHVFAIDDES 151
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

186 LMGGGFL-----FHWGVIDYCGGYVIHVSAGIAGFTAAVYVGPRAQKDERFPNNILFT 240
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 152 GYVGGMKNVLEFH----DFAGCTAVHNMNAGASGLAIALIVGRHSM---AVRPHNLPLI 204
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

241 LTGGLLMWGAAGNGGFPYANSVASMAVLTNTICITAMSLIVTCTDVIFFKKRSVYGA 300
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 205 LIGAGLIVAGWFGFNGGTAGGANPLASTVVTSLIAAGGMMGFMLVERVFSKPTFFGS 264
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

301 VQGMITGLVCTTPAGVYQGWALVMGVLAGSIPWYTMIIHKESKILQRYDDTLGVFHT 360
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 265 ATGTITAGVATTPAADAVSPIGAFVAGLGVAFSFWA--ISMKG---HRVDDSPDVAV 319
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

361 HGVAGLGGLLTGLPAEBTLCNPLPVADSRGAFYGGAGQAFGKQIAGSLFVAVANVYV 420
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 320 HGMAGIAGALFVMLFGDP-----LAPAGVSGVFEGGELSLIMREPLA-IIVTLTYAFGV 372
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

421 TSLICLAINLVPLRMPPD-KLEVGDPAVHGEBAVYALMGDG 460
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 373 TWLIATITLTKMTJRTISEAYEGIDREHSAESHLSNG 413
   : : | : | : | : | : | : | : | : | : | : | : | : | : | : |

RESULT 12
US-09-487-558B-192
; Sequence 192, Application US/09487558B
; Patent No. 6949356
; GENERAL INFORMATION:
; APPLICANT: Busby, Robert
; APPLICANT: Call, Brian
; APPLICANT: Hecht, Peter
; APPLICANT: Holzman, Doug
; APPLICANT: Madden, Kevin
; APPLICANT: Maxon, Mary
; APPLICANT: Milne, Todd
; APPLICANT: No. 6949356man, Thea
; APPLICANT: Royer, John
; APPLICANT: Salama, Sofie
; APPLICANT: Sherman, Amir
; APPLICANT: Silva, Jeff
; APPLICANT: Summers, Eric
; TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
; FILE REFERENCE: 109272.110
; CURRENT APPLICATION NUMBER: US/09/487,558B
; PRIOR APPLICATION NUMBER: US 60/487,558
; PRIOR FILING DATE: 1999-10-20
; NUMBER OF SEQ ID NOS: 446
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 192
; LENGTH: 492
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
; US-09-487-558B-192

Query Match      18.7%; Score 474.5; DB 2; Length 492;
Best Local Similarity 26.2%; Pred. No. 1.1e-38;
Matches 132; Conservative 87; Mismatches 205; Indels 79; Gaps 13;

4 SATVVPL---AYQGTSAVSADMLKNGNAMOVLVATVGLVSVGLVVLVYGVVKKKVA 60
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 3 SRTTGPLTTEYTDGFTV-----AFMILGALVFFM-VFGLGFLVSLGARRKSA 49
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

61 VNSAFMALYAFAPAAVVICWTVAYNNSFGEKLLPIWGKARPALDOGLLVGRALPATVHYR 120
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 50 LALIVVLMATVIGLQVYFWGYSIAF-----SKSAP-----NNK 84
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

121 ADGSVETAAV-----EPLYPMATVYVYQCVFAATILLVAGSLIGRMSFLAMMIFV 171
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 85 FTGNLDSFGFRNVYKKEDEDAVPELAYATFQMFSVNLISIIAGATAERGRLLPHWVFL 144
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
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QY 172 PLMLTSTYVGAFLWG--GGFLFMGVIDYCGGVIVHSAGINGFTAAVWGPRAQDR 230
DB 145 FILATIGCPVYTWISPGGMAYQWGLWAGGNGEILLSAVSGFYVSWFLGRNEKLLI 204
QY 231 REPNNILFLTLAGLLMGMAGFNGGPPAANSVASMALVNTNICTAMSLIWTCLDYI 290
DB 205 NRRPHVSLVLTGSLTLMFGMLFNSASSLPRLRSYAFAMTCLSAITGCMWCLDPR 264
QY 291 FFKPSVGAQVGMITGLVCTPAGVVGMAALVNGVLASIPWYTMILHRSKILOR 350
DB 265 SEKKMSTVGLCSGIIISGLVATPSSGCTILYSLIGIYAGVVCNPFATKL-----KYAK 319
QY 351 VDDTLGVFHTGIVAGLLGLLTGLFAEPTLCNLFPLVADSRGAPYGG---AGAAQFGKOI 407
DB 320 VDDAMPDILAEHGVAGVIGLIFNALFGADVIGM-----DGTTEHGGWTHNYKQYKOI 374
QY 408 AGGLFVAVMNVVTSICLAINLLVPLR-----MPDDKL-EVGDVAHGEEAAY 455
DB 375 AYTAASIGYTAAYTAIICFVLGTYIPGMRLISEAEAGDEDOIGEFADYVEVRDYY 434
QY 456 LMG---DGEWYDVKHGSAAVA 475
DB 435 LMGVDEDSQSDVNHVYNAHLA 457

RESULT 13
US-08-635-967-2
; Sequence 2, Application US/08635967
; Patent No. 6620610
; GENERAL INFORMATION:
; APPLICANT: FROMMER, Wolf-Bernd
; APPLICANT: NINEMAN, Olaf
; TITLE OF INVENTION: DNA SEQUENCES FOR AMMONIUM TRANSPORTER,
; TITLE OF INVENTION: PLASMIDS, BACTERIA, YEASTS, PLANT CELLS AND PLANTS
; TITLE OF INVENTION: CONTAINING THE TRANSPORTER
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ostroienk, Faber, Gerb & Soffen, LLP
; STREET: 1180 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10036-8403
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Releasee #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/635,967
; FILING DATE: 29-APR-1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP 94/03499
; FILING DATE: 24-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 43 37 597.9
; FILING DATE: 28-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weilmann, Edward
; REGISTRATION NUMBER: 24,735
; REFERENCE/DOCKET NUMBER: P/951-120
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 382-0700
; TELEFAX: (212) 382-0888
; TELEX: 236925
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 501 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-635-967-2

Query Match 13.4%; Score 338.5; DB 2; Length 501;
Best Local Similarity 25.7%; Pred. No. 4,5e-25;
Matches 134; Conservative 64; Mismatches 220; Indels 103; Gaps 18;

QY 1 MESSATVPLAVQNTSAS-----VADMLKGS-----DNAMQVATVIGLQSVG 46
DB 1 MGSATDVLAVLGPATTAANYICGQLGDNKKFIDTAIPADINTYLLFSAIYVFSQQL-G 59
QY 47 LVVLGGVVKKKMAVNSAFMALYAPAAVVICWYAAVYNSFSEKLLPIWGKAPALDQGL 106
DB 60 FAMLGAGVRAKNTVMIMLTNVLDAAGLFFYLLFGYAPAFSPSNGFIGK----- 110
QY 107 LVGRALPATVHYRADSGVETAAVEPLVPMATVVVFOCPAAITLLIVAGSLGKMSFLA 166
DB 111 -----HYFGIKDIPITASD-----YSNFLYQMAFALAAAGITSGSIAERTQFVA 154
QY 167 WMIFVPLMLTFSYTVGAFSLWG-----GGFLFMGVIDYCGGVIVHSAGIAGF 215
DB 155 YLIISSFLTGFYIPVYSHFMSVYDGWASPPRTDGLLFSTGALDPAAGSVHMGSIAGL 214
QY 216 TAAVWGPRAQDRERFPNNILFTLTGAG-----LWMGVAENG----- 257
DB 215 WGLALIEGPRL---GRFNGGRALALRGHSASLVLTGFTLWFGWYGFNPGSFNKILVTV 270
QY 258 --GPYAA--NSVASNAVLTNICTAMSLIWTCLDYIFPKRP-----SVGAVQGMING 307
DB 271 ETGTVNGQMSAVGRTVITTLTLAGCTA-----ALTTLFGKLLSGHNVTVDCNGLLGG 323
QY 308 IVCITPAGVVGMAALVNGVLASIPWYTMILHRSKILOR--DPLGVFHTHGVAG 365
DB 324 FAITGGCSVVEPMALITGFVAA-----LVLAGCNLAERKATKDDLEAAQLHGCGG 376
QY 366 ILGSLITGLFAEPTLCNLFPLVADSR--GAFYGAAGAGFOGQIAGLFLVAMNVVTSI 423
DB 377 AMGLITFALFAQEKYINQYGNKPGPHGLFMNG--GKLLGALQLIIVITGVASATMGT 435
QY 424 ICLAINLVPLRM-PDDKLEVGDDVAHGEEAVALMGDGMY 463
DB 436 LFFILKKMKLRISSDEMAAGMDMTRHGGFAVYMPDDDESH 476

RESULT 14
US-09-134-000C-5907
; Sequence 5907, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 5907
; LENGTH: 361
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
; US-09-134-000C-5907

Query Match 13.2%; Score 335; DB 2; Length 361;
Best Local Similarity 24.9%; Pred. No. 6.4e-25;
Matches 98; Conservative 69; Mismatches 155; Indels 72; Gaps 10;

QY 46 GLVLIYGVVKKKKMAVNSAFMALYAPAAVVICWYTAVMNSFGEKLLPIWGKAPALDQGL 105
DB 24 GVLIYVGLVNHRYIHHTLILGLVTLISGTLCLMFLVGYSLSF-----FGN----- 68
QY 106 LLVGRALPATVHYRADSGVETAAVEPLVPMATVVVFOCPAAITLLIVAGSLGKMSFL 165

[illegible]

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RESULT 15
US-10-033-109-4
Sequence 4, Application US/10033109
Patent No. 6833492
GENERAL INFORMATION:
APPLICANT: Allen, Stephen M.
APPLICANT: Rafalski, J. Antoni
APPLICANT: Sakai, Hajime
TITLE OF INVENTION: Nitrogen Transport Metabolism
FILE REFERENCE: BB-1210
CURRENT APPLICATION NUMBER: US/10/033,109
CURRENT FILING DATE: 2001-12-28
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/384,623
PRIOR FILING DATE: EARLIER FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/098,248
PRIOR FILING DATE: EARLIER FILING DATE: 28 August 1998
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Microsoft Office 97
SEQ ID NO 4
LENGTH: 500
TYPE: PRT
ORGANISM: Glycine max
US-10-033-109-4

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Query Match 12.4%; Score 313.5; DB 2; Length 500;
 Best Local Similarity 24.7%; Pred. No. 1.4e-22;
 Matches 119; Conservative 63; Mismatches 213; Indels 87; Gaps 15

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OY      28 DNAQMLVATVATLVLGLOSVPRLVVLVYGGVVKKKKAVNSAFALVYFAALVWVIMCWTMAVNAI 87
Db      48 DNTYLLFSAVLVYFNSQDL--GFAMLCAGSVAAKNTNMNIMLNTVIDAAAGGLFYLLFGAPAF 106
OY      88 GEKLLPTMGKARPALDQGLLVGRALLPVTYHRADGSVETAAVEPLYPMAVTYVPCVRA 147
Db      107 GSPSNGFIK-----HFGKLDIPSSSYDYSY-----FLYMAARA 141
OY      148 AITLLIVAGSLIGRMSFLAMMIFVPLMLTFSYVGAFLS-----MGGF-----LPRMGV 197
Db      142 IAAAGITSSISMERQFVAIVLLYSFLTGEPVYRVVSHWFMSPDGMASAFLLIDRLSTGY 201
OY      198 IDYCGGYVLHVNSAGLNGFTPAATVWGPRAQDKRFRP-----ENIILFTITGGLIM 248
Db      202 IDFASGVVHWMIAGLWGLALIEGR---MGRFDHAGRAVALRGHSASLVLLGTFLLM 257
OY      249 MGMAGF-----NGGPRYAANSVASMAVLTNTINCTAMSLIVTCTDVIFFPKR 295
Db      258 FGMVGFNPSPFKKILLITVYNSGNYQGMBAVGRTAATTTLAGSTA-----ALTTLLGKV 312
OY      296 ----SVGAVQGMITGLVCTIPDAGVQGMALVMGVLAGSIPTWTMMILHKRSKILOR 350

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Db 313 ISGHMNTDVCGNLLGGFAAITAGCSVYEPMAIYCGFVAS-----IYLINCKLAEK 365

QY 351 V--DDTGVFHTHGVAAGLIGLLTGI,FABPITCLN,FLPVADSRGAFYGAGAGQFGKQIA 408

Db 366 VKRDPDLEAAQHLHGCGGTGWI,FTLLFAKKEVKEVYVGLGSAHGLMGG--GKLLAAHVI 424

QY 409 GGFVVAAMVVVTSLLCLAINLLVPLRM--PDDKLEVGDDAVHGEEAVALMGDMGYDVK 467

Db 425 QILVIAIGWVSATMGPLFMGLNKLKILRISSDELLAGMDTHGGFAIAYEDD----ETHK 480

QY 468 HG 469

Db 481 HG 482

Search completed: July 22, 2006, 03:34:39
Job time : 52 secs

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: July 23, 2006, 19:25:14 ; Search time 20323 Seconds
(without alignments)
11569.880 Million cell updates/sec

Title: US-10-713-648a-29

Perfect score: 3677
Sequence: 1 aaataaaacataagfca.....aagctccatatttccaaa 3677

Scoring table: IDENTITY NUC
Gapop 10_0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

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1: gb_env:*
2: gb_pat:*
3: gb_ph:*
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6: gb_ro:*
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8: gb_sy:*
9: gb_un:*
10: gb_vl:*
11: gb_ov:*
12: gb_hcg:*
13: gb_in:*
14: gb_om:*
15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2541.6	69.1	110000	4 AP008209_350	Continuation (351
2	2541.6	69.1	171376	4 AC104487	AC104487 Oryza sat
3	746.4	20.3	1790	4 AK100411	AK100411 Oryza sat
4	733.6	20.0	1441	4 AK069311	AK069311 Oryza sat
5	529.2	14.4	1656	2 AR628380	AR628380 Sequence
6	529.2	14.4	1656	4 BT009273	BT009273 Triticum
7	528.2	14.4	1521	4 AY428038	AY428038 Triticum
8	454	12.3	1577	4 AB083582	AB083582 Oryza sat
9	454	12.3	4067	4 AK120352	AK120352 Oryza sat
10	454	12.3	110000	4 AP008207_377	Continuation (378
11	454	12.3	148892	4 AP003235	AP003235 Oryza sat
12	392.6	10.7	5153	4 AB083581	AB083581 Oryza sat
13	392.6	10.7	110000	4 AP008207_355	Continuation (356
14	392.6	10.7	110000	4 AP008211_228	Continuation (229
15	392.6	10.7	114236	4 AC112159	AC112159 Oryza sat
16	392.6	10.7	143515	4 AP003252	AP003252 Oryza sat
17	389.2	10.6	1140	4 AK109023	AK109023 Oryza sat
18	389.2	10.6	1883	2 AR628378	AR628378 Sequence

19	388	10.6	1957	4 AK065288	AK065288 Oryza sat
20	388	10.6	2040	4 AB051864	AB051864 Oryza sat
21	385.4	10.5	1687	4 AK063959	AK063959 Oryza sat
22	385.4	10.5	1717	4 AK102106	AK102106 Oryza sat
23	375.6	10.2	110000	4 AP008208_207	Continuation (208
24	375.6	10.2	137046	4 AP004775	AP004775 Oryza sat
25	372.6	10.1	1870	4 AK108711	AK108711 Oryza sat
26	344.8	9.4	110000	4 AP008217_002	Continuation (3 of
27	344.8	9.4	160673	4 CNG08BCDR	BX000501 Oryza sat
28	336.8	9.2	96667	4 CNG08BCDH	BX000491 Oryza sat
29	336.8	9.2	110000	4 AP008218_002	Continuation (3 of
30	290	7.9	98153	12 AC174314	AC174314 Medicago
31	290	7.9	124043	4 AC140029	AC140029 Medicago
32	289.6	7.9	1961	2 AR628379	AR628379 Sequence
33	273	7.4	1655	4 AF187962	AF187962 Lotus jdp
34	215.4	5.9	1658	4 AF182039	AF182039 Arabidops
35	207.4	5.6	135334	4 AC146554	AC146554 Medicago
36	207.2	5.6	1818	4 AY122328	AY122328 Medicago
37	195.6	5.3	81467	4 AC004683	AC004683 Arabidops
38	195.6	5.3	115359	4 AC003028	AC003028 Arabidops
39	190.2	5.2	376	2 AR628377	AR628377 Sequence
40	176.4	4.8	110000	4 AP008209_306	Continuation (307
41	176.4	4.8	139872	4 AC091811	AC091811 Oryza sat
42	167.8	4.6	110000	4 AP008207_243	Continuation (244
43	167.8	4.6	166753	4 AP002866	AP002866 Oryza sat
44	137.6	3.7	110000	4 AP008212_039	Continuation (40 o
45	137.6	3.7	153749	4 AP003019	AP003019 Oryza sat

ALIGNMENTS

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Sequence split into 362 fragments LOCUS AP008209 Accession AP008209				
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Best Local Similarity	85.2%	Pred. No. 0;		
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QY	166	CAAGCGAGTCAAAATGGTTAATCGATCGCACTGACATGATCATCTCTATATAT----	221	
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DB	24408	ATATTAAGCTGCTCACTTAACACTTAATCTGATGATCAAAATTAACAAATTAACACTT	2446	
QY	276	AGTGTGTGTTAAATACAGCGAAGAAATGTGTCGTCCGCGAGCGGTGCGCGTGGGCTA	335	
DB	24468	AGTGTGTGTTAAATACAGCGAAGAAATGTGTCGTCCGCGAGCGGTGCGCGTGGGCTA	2452	
QY	336	CCAGGGGACACGTCGCGCTGCTGCGTGGCGA CTGGCTGAACAAGGGGGACAAAGCGTGGCA	395	
DB	24528	CCAGGGGACACGTCGCGCTGCTGCGTGGCGA CTGGCTGAACAAGGGGGACAAAGCGTGGCA	2458	
QY	396	GCTGTGTGGCGCGACGCTGTGTGGGGCTTGCAGAGCGTGCAGAGCGTGCAGAGCGTGCAGAG	455	
DB	24588	GCTGTGTGGCGCGACGCTGTGTGGGGCTTGCAGAGCGTGCAGAGCGTGCAGAGCGTGCAGAG	2464	
QY	456	CGGGTGTGTGAAGAAGTGGGGCGTGAATCGCGCTTCAATGGCGCTTACAGCGCTTACAG	515	
DB	24648	CGGGTGTGTGAAGAAGTGGGGCGTGAATCGCGCTTCAATGGCGCTTACAGCGCTTACAG	2470	
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DB	24708	CGCGGTGTGTGCTGTGCTGGGTCACTTGGGGCTTACAAATGTCTTGGGGGAGAACTCT	2476	
QY	576	CCCGATCTGGGGGAAAGCGCGCGCGCTGGAACCAAGGGCTCTCTGTGTGGCGCGCGCG	635	
DB	24768	CCCGATCTGGGGGAAAGCGCGCGCGCGCTGGAACCAAGGGCTCTCTGTGTGGCGCGCGCG	2482	
QY	636	GCTGTGGGGACGCTTCCATCACTCCGCGCGGACGCTGGAACCGGTGGGTGGAGCC	695	
DB	24828	GCTGTGGGGACGCTTCCATCACTCCGCGCGGACGCTGGAACCGGTGGGTGGAGCC	2488	
QY	696	GCTGTACCCGATGGGACGAGTGGTGAATTCACAGTGCATTTGGCGGACATCACTTCAT	755	
DB	24888	GCTGTACCCGATGGGACGAGTGGTGAATTCACAGTGCATTTGGCGGACATCACTTCAT	2494	
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[illegible]

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Db	27499	CCTGGGGGGGCGCTCTCTCAACGGGCGCTTGGCGAGGCCACCTCTTTCGACCTCTTCTCC	27555
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DEFINITION	Oryza sativa chromosome 3 BAC OSUNBa0042109 genomic sequence,	PLN 15-FEB-2003	
ACCESSION	AC104487		
VERSION	AC104487.3		
KEYWORDS	HTG.		
SOURCE	Oryza sativa (japonica cultivar-group)		
ORGANISM	Oryza sativa (japonica cultivar-group)		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
AUTHORS	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP		
	clade; Euhartoidae; Oryzeae; Oryza.		
	1 (bases 1 to 171376)		
	Buell, C.R., Yuan, Q., Ouyang, S., Liu, J., Gansberger, K., Jones, K.M.,		

TITLE	JOURNAL
REFERENCE	Unpublished
AUTHORS	2 (bases 1 to 171376)
TITLE	Buell,R.
JOURNAL	Direct Submission
REFERENCE	Submitted (12-DEC-2001) The Institute for Genomic Research, 9712
AUTHORS	Medical Center Dr, Rockville, MD 20850, USA
TITLE	3 (bases 1 to 171376)
JOURNAL	Buell,R.
REFERENCE	Direct Submission
AUTHORS	Submitted (07-FEB-2003) The Institute for Genomic Research, 9712
TITLE	Medical Center Dr, Rockville, MD 20850, USA
JOURNAL	4 (bases 1 to 171376)
REFERENCE	Buell,R.
AUTHORS	Direct Submission
TITLE	Submitted (14-FEB-2003) The Institute for Genomic Research, 9712
JOURNAL	Medical Center Dr, Rockville, MD 20850, USA, rbuell@tigr.org
REFERENCE	5 (bases 1 to 171376)
AUTHORS	Buell,R.
TITLE	Direct Submission
JOURNAL	Submitted (15-FEB-2003) The Institute for Genomic Research, 9712
REFERENCE	Medical Center Dr, Rockville, MD 20850, USA, rbuell@tigr.org
AUTHORS	On Feb 7, 2003 this sequence version replaced gi:18497084.
TITLE	Address all correspondence to:rice@tigr.org
JOURNAL	
COMMENT	BAC clone OSUNBa0042109 is from Oryza sativa chromosome 3 The orientation of the sequence is from SP6 to T7 end of the BAC clone. Genes were identified by a combination of several methods: Gene prediction programs including Fgenesh (http://www.softberry.com/), genscan and Genscan+ (Chris Burge, http://CCK-001.mit.edu/GENSCAN.html), GenemarkHM (Mark Borodovsky, http://genomeark.biology.gatech.edu/Genemark/), and GenspliceR (Michael Pereira and Steven Salzberg, contact mperae@tigr.org), searches of the complete sequence against a peptide database and the plant EST database at TIGR (http://www.tigr.org/cdb/cgi.shtml) Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity are named as unknown proteins Genes without protein or EST similarity, that are predicted by more than two gene prediction programs over most of their length are annotated as hypothetical proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, http://genome.wustl.edu/eddy/tRNAscan-SE/). Simple repeats are identified by repeatmasker (Arian Smit, http://ftp.genome.washington.edu/RM/repeatmasker.html). This BAC overlaps with rice BAC OSUNBa0096106 (AC092557) and OSUNBa0075ML2 (AC096856).
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QY 2137 TGAACAAATACAAAGCTTCATCG-----TATCTCTCTCACTCTCTGTAGTGAAGA 2159
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QY 2160 -----GAATCTAGTGTGTTGAT 2177
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QY 2178 GCA-TACATATTTGCTCCGAACACAGAAATCTTATTTGTGCTTATGCTTAATGCTAATG 2236
DB 78996 GTAGTACATATTTGCTCCGAACACAGAAATCTTATTTGTGCTTATGCTTAATGCTAATG 78943
QY 2237 ACAATGCTATGCTAGTGTGCTAGTACTTAAGTCAAGAGTGTGCAAGTGTGCAAT 2296
DB 78942 -CAATGCTATGCTAGTGTGCTAGTACTTAAGTCAAGAGTGTGCTGCAAGTGTGCAAT 78884
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Db	77517	GCGGGTGGAGCTTTTAGGATATGCACTTGGAGATGACGGGAGTCGGTTCGTAT	77512
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Oy	3632	AAGGTAAATATATATTTGTTATTAAGCTCCATATTTCCAAA	3677
Db	77457	AAGGTAAATATGTTATTTGTTATTAAGCTCCATATTTCCAAA	77412
RESULT 3			
LOCUS	AK100411	1790 bp	mRNA linear
DEFINITION	Oriza sativa (japonica cultivar-group) cDNA clone:U023087J01, full insert sequence.		
ACCESSION	AK100411		
KEYWORDS	FLJ_CDNA; CAP trapper.		
SOURCE	Oriza sativa (japonica cultivar-group)		
ORGANISM	Euryzoota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BBP clade; Euharoidae; Oryzeae; Oryza.		
REFERENCE	1		
AUTHORS	The Rice Full-Length cDNA Consortium, National Institute of Agricultural Sciences Rice Full-Length cDNA Project Team; Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yanagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group; Otsomo, Y., Murakami, K., Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y., Kurosaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M., Nakikawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Nikura, J., Ikeda, R., Ishibiki, J., Kawamata, M., Yoshimura, A., Miura, J., Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matubara, K., RIKEN, Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashidume, W., Hayatsu, N., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kondo, S., Kono, H., Miyazaki, A., Oosato, N., Ota, Y., Sato, R., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Yoshino, M. and Hayashizaki, Y.		
TITLE	Yoshino, M. and Hayashizaki, Y.		
JOURNAL	Japconca rice		
PUBMED	Science 301 (5631), 376-379 (2003)		
REFERENCE	12869764		
AUTHORS	2 (bases 1 to 1790)		
	Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K., Fujimura, T., Fukuda, S., Hanesaki, T., Hara, A., Hashinume, W., Hayashida, K., Hayashizaki, Y., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Hotta, I., Iida, Y., Ikeda, R., Imamura, K., Imotani, K., Ishibiki, J., Ishii, Y., Ishikawa, M., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawagashira, N., Kawai, J., Kawamata, M., Kikuchi, S., Kishikawa-Hirozane, T., Kishimoto, N., Kobayashi, M., Kodama, T., Kojima, K., Kojima, Y., Kondo, S., Kono, H., Kouda, M., Koya, S., Kurihara, C., Kurosaki, T., Kusumegi, T., Li, C., Lu, M., Masuda, H., Matsubara, K., Matsumura, T., Miura, J., Miyazaki, A., Mizuno, K., Murakami, K., Murata, M., Nagata, T., Nakamura, M., Nanki, T., Narikawa, R., Nikura, J., Nishi, K., Nomura, K., Numasaki, R., Ohneda, E., Ohno, M., Ohsaki, K., Oka, M., Ooka, H., Oosato, N., Ota, Y., Otsomo, Y., Ryu, R., Satoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Satoh, K., Shibata, K., Shinagawa, A., Shiraki, T., Shishiki, T., Sogabe, Y., Sugano, S., Sugiyama, A., Suzuki, K., Suzuki, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akashi, S., Tanaka, T., Tomaru, A., Toya, T., Tsunoda, Y., Ueda, M., Waki, K., Xie, Q., Yanagi, W., Yoshida, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomoto, S. and Yoshimura, A.		
TITLE	Direct Submission		
JOURNAL	Submitted (27-AUG-2002) Shoshi Kikuchi, National Institute of Agricultural Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail:skikuchi@nias.affrc.go.jp).		

	COMMENT	Tel:+81-29-838-7007, Fax:+81-29-838-7007) This clone is one of the 28K full-length cDNA clones from japonica rice.
	URL :	http://cdna01.dna.affrc.go.jp/cDNA/ NIRS Rice Full-length cDNA Project Team: Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Iplikawa, M., Yamada, H., Ooka, H., Horita, I., Koijima, K., Namiki, T., Ohneda, E., Yanagi, W., Suzuki, K., Li, C., Onitsuki, K., Shihinki, T. and Yamamoto, M.
	FAIS Genome Sequencing & Analysis Group:	Otomo, Y., Iida, Y., Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M., Kodama, T., Kurotaki, T., Kusunegi, T., Lu, M., Masuda, H., Miura, J., Mizuno, K., Narikawa, R., Nikura, J., Oka, M., Ryu, R., Sugeno, S., Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S., Yoshimura, A., Matsubara, K. and Morakami, K.
	Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken:	Adachi, Y., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hangacki, T., Harai, A., Hashizume, W., Hayashida, K., Hayatsu, N., Himemoto, K., Hiroaka, T., Hori, F., Iida, J., Imamura, K., Imocani, K., Ishii, Y., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kamai, J., Kishikawa-Hirozane, T., Koijima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsumiya, T., Miyazaki, A., Murata, M., Nakamura, M., Niishi, K., Nomura, K., Numasaki, R., Ohno, M., Osato, N., Oca, Y., Saichou, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akashira, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K., Yaenishi, A. and Hayashizaki, Y.
	location/Qualifiers	
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Best Local Similarity	97.7%	Pred. No. 2.1e-153;
Matches 780;	Conservative 0;	Mismatches 11; Indels 7; Gaps 2;
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Dd	996	TGCAGGGGTGATGACAGGGGTGGGGCGCTTCGATGACAGGGGTGATGCCCGGACACATCCC 10555
Dy	2939	GTCGATACCACTGATGATTCCTCCACAAGAGCGTCCAATCCTTGAGCGCGTCAGACGACAC 2998
Dd	1056	GTCGATACCACTGATGATTCCTCCACAAGAGCGTCCAATCCTTGAGCGCGTCAGACGACAC 11155
Dy	2999	CCTCGGGCTTTCCACACCACCGGCGTGGCGGCTCTCTCGGCGGCTCTCTCACGGCGCT 3058
Dd	1116	CCTCGGGCTTTCCACACCACCGGCGTGGCGGCTCTCTCGGCGGCTCTCTCACGGGCTT 1175
Dy	3059	CTTGGCCGAGCCCACTCTTGCAACCTCTTCTCCCTGGCGCATCTCCGGGGCGCTT 3118
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Dy	3119	CTAAGCGGCGGCGCGGCGGCGCCACAGTTCCGGAACAGATGCGCGGCGGACTCTTCGTCGT 3178
Dd	1236	CTAAGCGGCGGCGCGGCGGCGCCACAGTTCCGGAACAGATGCGCGGCGGACTCTTCGTCGT 1295
Dy	3179	CGCCTGGAACGTCGTCGTCACTTCCCTCATCTGCTCGTCGCCATCAACTCTCTGTCGGCT 3238
Dd	1296	CGCCTGGAACGTCGTCGTCACTTCCCTCATCTGCTCGTCGCCATCAACTCTCTGTCGGCT 1355
Dy	3239	CCGCAATGCCGACGACAAAGCTCGAGGTCGGCGACGACGCGCTCCAGCGCGAGAGGCTTA 3298
Dd	1356	CCGCAATGCCGACGACAAAGCTCGAGGTCGGCGACGACGCGCTCCAGCGCGAGAGGCTTA 1415
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Dd	1416	CGCCTCTCGGGCGGACGCGGCGAGATGTCAGATCAACCAAGAAGAGGCTCCAGCGCGCGCT 1475

[illegible]

RESULT 5				
LOCUS	AR628380			
DEFINITION	AR628380	1656 bp	linear	PAT 14-FEB-2005
ACCESSION	Sequence 13	from patent US 6833492.		
VERSION	AR628380			
KEYWORDS	AR628380.1	GI:59751057		
SOURCE	Unknown.			
ORGANISM	Unknown.			
REFERENCE	1	Unclassified.		
AUTHORS	1	(bases 1 to 1656)		
TITLE	Allen, S.M., Rafalski, J.A. and Sakel, H.			
JOURNAL	Nitrogen transport metabolism			
FEATURES	Patent: US 6833492-A 13 21-Dec-2004;			
source	E. I. du Pont de Nemours and Company, Wilmington, DE			
	Location/Qualifiers			
	1..1656			
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	/mol_type="genomic DNA"			
ORIGIN				

Query Match	14.4%	Score 529.2	DB 2	Length 1656
Best Local Similarity	86.9%	Pred. No. 1.5e-105		
Matches 582, Conservative	0	Mismatches 88	Indels 0	Gaps 0

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QY 366 CTGCGTGAACAAAGGAGGACAAACGCGTGGCGAGCTGGCGCGGACGCTGTGGGGCTGCA 425
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QY	426	GAGGTCGCCGGCTGGTGGTGCCTGACGGCGGTGGTAAAGAAAGTGGCGGTGAA	495
Db	203	GAGGTCCCGGGACATGGTGTGGTCTGACGGGGGGGTGTAAAGAAAGTGGCGGTGAA	262
QY	486	CTCGGCTTACATGAGCGGCTTACGGCTTCGGCGCGGTGTGATCTGCTGGGTCACTTGGGC	545
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QY	546	GTACACATGTGTTTGGGGAGAAAGCTTCTCCGATCTGGGGGAAAGGCGCGCGGCT	605
Db	323	CTACACATGTGCTTCGGCGAGAGCTGCTCCGCTTCGGGGGCAAGGCCGGCCGGGCT	382
QY	606	GGACACGAGGCTCTCGTCGCGCGCGCGCGCGGCGTGGCGACGGTCCACTACCGCGCGA	665
Db	383	CGACCTAGGCTTCTCTGTCGCGCGCGCTCGCTCCGGCAACCGCGCATACCGCGAGA	442
QY	666	CGGACGCGTGAAGACGGCGGGGTGGAGCGGCTGTACCGATGGCGAGCGGTGTGTACTT	725
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QY	846	CGCCTTCTCCCTCTGGGGCGCGGCTTCTCTTTCATCTGGGGCGTCAATGACTACTGGG	905
Db	623	CGCCTTCTCCCGTGTGGGGCGCGGCTTCTCTTTCATCTGGGGCGTCAATGACTACTGGG	682
QY	906	CGGCTACGTCATCCAGCTTTCGCGCGGCATGCGGCTTACCGCGCGCTTACTTGGGTCCG	965
Db	683	CGGCTACGTCATCCAGCTTTCGCGCGGCATGCGGCTTACCGCGCGCTTACTTGGGTCCG	742
QY	966	TACTTAACAGC 975	
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RESULT 6	BT009273	1656 bp	mRNA	linear	PLN 20-JUN-2003
LOCUS	BT009273				
DEFINITION	BT009273				
ACCESSION	BT009273				
VERSION	BT009273.1				
KEYWORDS	FLI CDNA.				
SOURCE	Triticum aestivum (bread wheat)				
ORGANISM	Triticum aestivum				
REFERENCE	Eurycotla, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Pooidae; Triticeae; Triticum.				
AUTHORS	1 (bases 1 to 1656)				
TITLE	Tinger, S.V., Wolters, P., Powell, W., Dolan, M., Miao, G.-H., Caraher, N.R., Hanatey, M.K. and Hainey, C.F.				
JOURNAL	Direct Submission				
USA	Submitted (20-JUN-2003) Crop Genetics, E. I. DuPont de Nemours and Company, 1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104,				

FEATURES	SOURCE	LOCATION/QUALIFIERS
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Query Match	14.4%	Score 529.2	DB 4	Length 1656
Best Local Similarity	86.9%	Pred. No. 1.5e-105		
Matches 582; Conservative	0	Mismatches 88	Indels 0	Gaps 0

Db 623 CATCCACATCCCGCGCGCTTCAACCGCGGCTACTGGGTCGGCAAGAC 682
QY 975 C 975
Db 683 C 683

RESULT 8
AB083582 1577 bp mRNA linear PLN 07-MAR-2003
LOCUS Oryza sativa (japonica cultivar-group) OsAMT2;2 mRNA for ammonium transporter, complete cds.
DEFINITION
AB083582
ACCESSION
AB083582
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL

1
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukariyocae; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BBP
clade; Ehrhartoideae; Oryzace; Oryza.
Suenaga, A., Moriya, K., Sonoda, Y., Ikeda, A., Von Wieren, N.,
Hayakawa, T., Yamaguchi, T., and Yamaya, T.
Constitutive Expression of a Novel-Type Ammonium Transporter OsAMT2
in Rice Plants
Plant Cell Physiol. 44 (2), 206-211 (2003)
12610225
2 (bases 1 to 1577)
Suenaga, A., Yamaya, T., and Hayakawa, T.
Direct Submission
Submitted (11-APR-2002) Toshihiko Hayakawa, Tohoku University,
Graduate School of Agricultural Science, Department of Applied
Plant Science, Laboratory of Plant Cell Biochemistry,
Teusumidori-Akamiyamachi 1-1, Aoba-ku, Sendai, Miyagi 981-8555,
Japan [E-mail: toshi@biochem.tohoku.ac.jp, Tel: 81-22-717-8789,
Fax: 81-22-717-8789]
Location/Qualifiers
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ORIGIN
3' UTR

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QY 360 GCGGACCTGCTGAAACAAGGGGACACAAGCGTGGACACTGGTGGCGGGAAGCTGTGGG 419
Db 94 GCGGAGTGGCTGAAACAAGGGGACACAAGCGTGGACACTGGTGGCGGGAAGCTGTGGG 153
QY 420 GCTGACAGACGTCGCGGCTTGTGTGCTGTACGACGCGCGCTGTGTGAAGAAGTGTGGC 479
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RESULT 9
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LOCUS Oryza sativa (japonica cultivar-group) cDNA clone:J01306B21, full
DEFINITION
insert sequence.
ACCESSION
AKI20352
AKI20352.1 GI:37989975
VERSION
FLI CDNA; CAP trapper.
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Bukariyocae; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BBP
clade; Ehrhartoideae; Oryzace; Oryza.

REFERENCE
1 The Rice Full-Length cDNA Consortium. National Institute of
Agricultural Sciences Rice Full-Length cDNA Project Team.
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Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I.,
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Ohtsuki, K., Shishiki, T., Foundation of Advancement of International
Science Genome Sequencing & Analysis Group; Oromo, Y., Murakami, K.,
Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tanuda, Y.,
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RESULT 11
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ACCESSION AP003235 BA000010
VERSION AP003235.2 GI:13699092
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BBP
clade; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE
AUTHORS
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Yano, M., Jiang, J. and Gojobori, T.
The genome sequence and structure of rice chromosome 1
Nature 420 (6913), 312-316 (2002)
12447438
2 (bases 1 to 148892)
Sasaki, T., Matsumoto, T. and Yamamoto, K.
Direct Submission
Submitted (19-PEB-2001) Takuji Sasaki, National Institute of
Agrobiological Sciences, Rice Genome Research Program, Kannondai
2-1-2, Tsukuba, Ibaraki, 305-8602, Japan
(E-mail:tsasaki@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/,
Tel:81-298-38-7441, Fax:81-298-38-7468)
On Apr 19, 2001 this sequence version replaced gi:13027265.
Genes were predicted from the integrated results of the following:
GENSCAN (http://CCR-081.mit.edu/GENSCAN.html), FGENESH
(http://www.softberry.com/), GeneMark.hmm
(http://opal.biology.gatech.edu/GeneMark/), Glimmer
(http://www.tigr.org/cdb/glimmer/glimmer_form.html), RiceHMM
(http://xrp.dna.affrc.go.jp/RiceHMM/), SplicePredictor
(http://bioinformatics.iastate.edu/cgi-bin/bp.cgi), sism4

(<http://globoin.cse.psu.edu/html/docs/s1ma.html>), gap2 (<http://www.tigr.org/software/galmerm/>), BLASTX and BLASTY. The genomic sequence was searched against NCBI Nonredundant Protein database, nr (<ftp://ncbi.nlm.nih.gov/blast/db/>) and the cDNA sequence database at RGP or DDBJ. Protein homologues of the coding regions were searched against NCBI Nonredundant Protein database with BLASTP. ESTs represent the identified cDNA sequences using BLASTN with the corresponding DDBJ accession no. and RGP clone ID. Full-length cDNAs represent the identified cDNA sequences using BLASTN with the corresponding DDBJ accession no. A gene with identity or significant homology to a protein is classified based on the protein name to indicate the homology level such as same name, 'putative-' and '-like protein'. A gene without significant homology to any protein but with full-length cDNA or EST homology (covering almost the entire length of partial sequence) is classified as an 'unknown' protein. A gene predicted by two or more gene prediction programs is classified as a 'hypothetical' protein according to IRGSP standard. A gene predicted by a single gene prediction program is also classified as a probable 'hypothetical' protein and is included as a miscellaneous feature of the sequence.

This orientation of the sequence is from SP6 to T7 of the PAC clone. The orientation of P003A07 clone has an overlap with P0677H08 (DDBJ: AP003286) clone at 5' end and an overlap with P0491F11 (DDBJ: AP004669) clone at 3' end. Detailed information on overlap and assembly quality together with annotation of this entry is available at <http://rgp.dna.affrcgo.jp/GenomeSeq.html>.

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Location/Qualifiers	
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mRNA
CDS

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Gene
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Db 1986 CTTACTGGGTCCGCTACTAACAGCTCATCTTTTGTATATCTATCATC 2038
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Db 91496 CCATTTCACAAAGTACTCTTGACAGGTGGGCCCGAGGCTGAAAGACGACAGGAGCGGTT 91437
OY 1272 CCCCCGAACATATATATCTTTTCAAGCTGACGGGGCAGGGGCTGTGTGATGGGGTGGGC 1331
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RESULT 14
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WPCOMMENT

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 DB 64601 GGGTGTGTGTGGCTTCCGCAATGGCTTGGGAGAGCTCTCCGATCTGGGGAGG 64660
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 QY 713 CGGTGTGTACTTCCAGTGGCTGTGGCGGCATCCGCTCATCTGTGGCGGCTCC 772
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 VERSION AC112159.2 GI:38146013
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 SOURCE Oryza sativa (japonica cultivar-group)
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BPP
clade: Euharicotidae; Oryzaceae; Oryza.

REFERENCE
AUTHORS
1 (bases 1 to 114236)
Chow,T.-Y., Hsing,Y.-I.C., Chen,C.-S., Chen,H.-H., Liu,S.-M.,
Chao,Y.-T., Chang,S.-J., Chen,H.-C., Chen,S.-K., Chen,T.-R.,
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Liu,H.-L., Li,Y.-F., Lin,S.-J., Lin,Y.-C., Wu,S.-W., Yu,C.-Y.,
Yu,S.-W., Wu,H.-P. and Shaw,J.-F.
Oryza sativa BAC OJ1058_C01 genomic sequence

TITLE
JOURNAL
Unpublished
2 (bases 1 to 114236)
Chow,T.-Y. and Hsing,Y.-I.C.

REFERENCE
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TITLE
JOURNAL
Submitted (20-FEB-2002) Institute of Botany, Academia Sinica, 128,
Section 2, Academia Road, Nankang, Taipei 11529, Taiwan
3 (bases 1 to 114236)
Hsing,Y.-I.C. and Chow,T.-Y.

REFERENCE
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JOURNAL
Submitted (29-MAR-2003) Institute of Botany, Academia Sinica, 128,
Section 2, Yien-chu-yuan Road, Nankang, Taipei 11529, Taiwan
4 (bases 1 to 114236)
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JOURNAL
Submitted (03-NOV-2003) Institute of Botany, Academia Sinica, 128,
Section 2, Academia Road, Nankang, Taipei 11529, Taiwan
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Chow,T.-Y. and Hsing,Y.-I.C.

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AUTHORS
TITLE
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Submitted (17-JUN-2004) Institute of Botany, Academia Sinica, 128,
Section 2, Academia Road, Nankang, Taipei 11529, Taiwan
On Nov 3, 2003 this sequence version replaced gi:18767243.
The nucleotide sequence of this BAC clone was generated by
combining Monarc and ASPEC-Taiwan sequencing data. The
orientation of the sequence is from Sp6 to T7 of the BAC clone.
Genes were predicted from the integrated results of the following:
BLASTN2.0, BLASTX2.0, GENSCAN (Chris Burge,
http://genes.mit.edu/GENSCAN.html), Genshes
(http://www.softberry.com/), Glimmer
(http://www.tigr.org/softdb/glimmer/glimmer.html), TWINSCAN
(http://www.cis.wustl.edu/) and Genesplizer
(http://www.tigr.org/tdb/Genesplizer/index.html). The sequence was
searched against the Swiss-Prot+TrEMBL protein database, the NCBI
plant EST database, the TIGR Rice Gene Index and the rice
full-length cDNA database (KOME,
http://cdna01.dna.affrc.go.jp/cDNA/). Annotated genes are named to
indicate the level of evidence for their annotation. Genes with
similarity to other proteins are named after the database hits.
Genes without significant peptide similarity but with EST
similarity are named as unknown proteins. Genes without protein or
EST similarity, that are predicted by more than two gene prediction
programs over most of their length are annotated as hypothetical
proteins. This clone overlaps with OJ1387_F08 (accession # AC108503)
and OSJNB0005E20 (accession # AC121364).
Location/Qualifiers

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Matches 500; Conservative 0; Mismatches 135; Indels 18; Gaps 1;

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OM nucleic - nucleic search, using sw model

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Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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15: geneseqn2006s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	662	18.0	1437	12	ADP09655
3	529.2	14.4	1656	8	AA153990
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7	417.4	11.4	1664	13	ADX52363
8	389.2	10.6	1883	8	AA153988
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13	279.6	7.6	977	11	ACL28017
14	269	7.3	976	13	ADX31669
15	248.2	6.8	974	13	ADX32599
16	238.2	6.5	1325	11	ACL29969
17	223.6	6.1	450	11	ACL33455
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19	190.2	5.2	376	15	AE16007	AE16007 Zea mays
20	182.8	5.0	583	13	ACN55220	ACN55220 Cotton an
21	164.6	4.5	520	11	ACL32813	ACL32813 Rice abio
22	135.2	3.7	2000	11	ACL35441	ACL35441 Rice etre
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ALIGNMENTS

RESULT 1	ADP09638	standard; DNA; 3677 BP.
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XX	ADP09638;	
AC	ADP09638;	
DT	26-AUG-2004	(first entry)
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DE	Rice ammonium transporter genomic DNA without the T-DNA insert Segid 29.	
XX		
KW	Rice; ammonium transporter; GUS; insertional mutagenesis;	
KW	beta-glucuronidase; biotic stress resistance; pesticide; herbicide;	
KW	plant; ds; hygromycin phosphotransferase; HGH; T-DNA; transfer-DNA.	
XX		
OS	Oryza sativa.	
XX		
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FT	FT	/tag= a
XX		/note= "Location of T-DNA insert in rice line IC-109-35"
PN	WO2004046357-A1.	
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PD	03-JUN-2004.	
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PF	14-NOV-2003; 2003WO-KR002461.	
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PR	15-NOV-2002; 2002US-0427166P.	
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PA	(POSC-) POSCO.	
XX	(POST-) POSTECH FOUNDD.	
PI	An G, Ryu C, Han J, Kang H, An K;	
XX		
DR	WPI: 2004-449751/42.	
DR	P-FSDB; ADP09672.	
XX		
PT	New organ preferential nucleic acids and polypeptides, useful in	
PT	producing rice plants with desired characteristics and which are	
PT	resistant to herbicide, plant pathogen, fungi, bacteria, virus, insect,	
PT	nematode, and stress.	

XX Claim 1; SEQ ID NO 29; 296pp; English.

PS This invention relates to a novel method of identifying nucleic acid
XX molecules, or fragments thereof, that are expressed in an organ
CC preferential manner in rice. Specifically, it refers to producing rice
CC cell lines that carry tagged genes modified by T-DNA/GUS based
CC insertional mutagenesis, where the GUS portion of the insert is the
CC promoterless beta-glucuronidase reporter gene that can only be expressed
CC when it is inserted into an active gene. The present invention describes
CC generating transformed rice lines containing transfer-DNA (T-DNA)
CC hygroscopic phosphotransferase (HPT). Accordingly, this method can be used
CC to produce rice plants with desirable characteristics including increased
CC grain yield and nutritional content, resistance to biotic stresses,
CC pest/diseases, herbicides or insects, altered morphology or improved
CC characteristics referring to shape, taste or cooking quality of the
CC grain. This polynucleotide sequence represents the genomic DNA of a rice
CC gene that will be T-DNA/GUS tagged for expression analyses, given in an
CC exemplification of the invention.

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Query Match 100.0%; Score 3677; DB 12; Length 3677;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3677; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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FH Key Location/Qualifiers
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XX 14-NOV-2003; 2003WO-KR002461.
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XX (POSC-) POSCO.
XX (POST-) POSTECH FOUND.
XX
XX An G, Ryu C, Han J, Kang H, An K,
XX
XX MPI; 2004-449751/42.
XX
XX P-PSDB; ADP09672.
XX
XX New organ preferential nucleic acids and polypeptides, useful in
XX producing rice plants with desired characteristics and which are
XX resistant to herbicide, plant pathogen, fungi, bacteria, virus, insect,
XX nematode, and stress.
XX
XX Claim 8; SEQ ID NO 46; 296pp; English.
XX
XX This invention relates to a novel method of identifying nucleic acid
XX molecules, or fragments thereof, that are expressed in an organ
XX preferential manner in rice. Specifically, it refers to producing rice
XX cell lines that carry tagged genes modified by T-DNA/GUS based
XX insertional mutagenesis, where the GUS portion of the insert is the
XX promoterless beta-glucuronidase reporter gene that can only be expressed
XX when it is inserted into an active gene. The present invention describes
XX generating transformed rice lines containing the selectable marker
XX hygromycin phosphotransferase (HPT). Accordingly, this method can be used
XX to produce rice plants with desirable characteristics including increased
XX grain yield and nutritional content, resistance to biotic stress,
XX pesticides, herbicides or insects, altered morphology or improved
XX characteristics referring to shape, taste or cooking quality of the
XX grain. This polynucleotide sequence represents the open reading frame DNA
XX of a rice gene that will be T-DNA/GUS tagged for expression analyses,
XX given in an exemplification of the invention.
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Best Local Similarity 99.3%; Pred. No. 3.1e-91;
Matches 665; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 301 ATGTGTCGTCGGCGACGCTGTGCGGCTGCGCTACCAAGGGAACAAGTCGCGTGGTG 360
DB 1 ATGTGTCGTCGGCGACGCTGTGCGGCTGCGCTACCAAGGGAACAAGTCGCGTGGTG 60
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DB 301 GCGCTGACACAGGCGCTCTCTGTCGCGCGCGCGCGCTGCGCGACGCTGCACTACCGC 360
QY 661 GCCACGCGACGCTGAGAGACGCGCGGCTGAGAGCGCGCTGACCGGATGAGCGAGGTG 720
DB 361 GCCACGCGACGCTGAGAGACGCGCGGCTGAGAGCGCGCTGACCGGATGAGCGAGGTG 420
QY 721 TACTTCAGTGCAGTGTGCGCGCATACCTCACTCTGTCGCGGCTCCCTCTCGGC 780
DB 421 TACTTCAGTGCAGTGTGCGCGCATACCTCACTCTGTCGCGGCTCCCTCTCGGC 480
QY 781 GCGATGACCTTCTTCGCGCTGATGATCTTGTCCGCGCTGTGCTACCTTCTCTACAC 840
DB 481 GCGATGACCTTCTTCGCGCTGATGATCTTGTCCGCGCTGTGCTACCTTCTCTACAC 540
QY 841 GTGCGCGGCTTCTCCCTGTCGCGCGCGCGCTTCTCTTCCACTGAGGCGTATGACTAC 900
DB 541 GTGCGCGGCTTCTCCCTGTCGCGCGCGCGCTTCTCTTCCACTGAGGCGTATGACTAC 600
QY 901 TCGGCGGCTACGTCATCCAGCTCCGCGCGCATGCGCGGCTTCAACCGCGCTTACTG 960
DB 601 TCGGCGGCTACGTCATCCAGCTCCGCGCGCATGCGCGGCTTCAACCGCGCTTACTG 660
QY 961 GTCCGTA 970
DB 661 GTGGGGCCAA 670

RESULT 3
AAL53990
ID AAL53990 standard; cDNA; 1656 BP.
XX
XX AAL53990;
AC 18-FEB-2003 (first entry)
DT
DE cDNA encoding a wheat high affinity ammonium transporter protein #2.
XX
XX Herbicide; ammonium transporter protein; herbicide; transgenic plant;
XX wheat; gene; ss.
XX
XX Triticum aestivum.
OS
XX
XX Key Location/Qualifiers
FH FT 93..1505
FT CDS /*tag= a
FT /product= "wheat high affinity ammonium transporter
FT protein"
XX
XX US2002142390-A1.
XX
XX 03-OCT-2002.
XX
XX 28-DEC-2001; 2001US-00033109.
XX
XX 28-AUG-1998; 98US-0098248P.
XX
XX 27-AUG-1999; 99US-00384625.
XX
XX (ALIE/) ALLEN S M.
XX (RAFA/) RAFALSKI J A.
XX
XX Allen SM, Rafalski JA;
XX
XX MPI; 2003-102520/09.
XX
XX P-PSDB; AAO26538.
XX
XX Novel ammonium transporter polypeptide useful for identifying enzymatic
XX inhibitors, which is homologous to corn, soybean, wheat or rice ammonium
XX transporter polypeptides.
XX
XX Claim 3; Page 23-24; 27pp; English.
XX
XX The invention relates to a novel ammonium transporter protein comprising

```


XX Rice abiotic stress responsive polynucleotide SEQ ID NO:2057.
 DE ss; abiotic stress tolerance; transgenic plant; plant; cereal;
 KM agriculture.
 XX Oryza sativa.
 OS WO2003008540-A2.
 PN 30-JAN-2003.
 PD 21-JUN-2002; 2002WO-US019668.
 PF 22-JUN-2001; 2001US-0300112P.
 PR 24-AUG-2001; 2001US-0314662P.
 PR 26-SEP-2001; 2001US-0325277P.
 PR 21-NOV-2001; 2001US-0332132P.
 XX (SYGN) SYNGENTA PARTICIPATIONS AG.
 PA Kreps J, Briggs SP, Cooper B, Glazebrook J, Goff SA, Katagiri F,
 PI Moughamer T, Provart N, Riecke D, Zhu T;
 XX WPI; 2003-248011/24.
 DR New stress-responsive nucleic acid, useful for altering the
 XX responsiveness of a plant, e.g. cereal, to an abiotic stress such as cold
 PT stress, salt stress or osmotic stress.
 PT Claim 1; SEQ ID NO 2057; 899p; English.
 PS The invention relates to novel abiotic stress responsive polynucleotides
 XX and polypeptides. Also disclosed are vectors, expression cassettes, host
 CC cells, and plants containing such polynucleotides. Also disclosed are
 CC methods for using the polynucleotides and polypeptides to alter the
 CC responsiveness of a plant to abiotic stress. The invention is useful in
 CC agriculture. The nucleic acid is useful for determining whether a test
 CC plant has been exposed to an abiotic stress condition. It is also useful
 CC for selecting an agent that alters abiotic stress regulated
 CC polynucleotide expression in a plant cell, and to identify a homolog or
 CC ortholog to an abiotic stress responsive polynucleotide. The nucleic acid
 CC molecule and the polypeptide encoded by it are useful in altering the
 CC responsiveness of a plant to an abiotic stress, such as cold stress, salt
 CC stress, osmotic stress or any of their combinations. The present sequence
 CC is used in the exemplification of the invention
 XX
 XX Sequence 978 BP; 145 A; 321 C; 320 G; 191 T; 0 U; 1 Other;
 SQ
 Query Match 12.3%; Score 453; DB 11; Length 978;
 Best Local Similarity 81.8%; Pred. No. 1.6e-59;
 Matches 554; Conservative 0; Mismatches 105; Indels 18; Gaps 2;
 QY 301 ATGTCTGTCGCGGCGAGCGTGTGCGGCGTGAACGAGGGAACAGTGGCGTGG 360
 DB 1 ATGTCTGCGGCGAGCGTGTGCGGCGTGAACGAGGGAACAGTGGCGTGG 57
 QY 361 GCGGAGTGGCTGAACAAGGCGGGAACAAGCGTGGAGCTGTGGCGGCGAGCTGTGG 420
 DB 58 CCGGAGTGGCTGAACAAGGCGGGAACAAGCGTGGAGCTGTGGCGGCGAGCTGTGG 117
 QY 421 CTGCAGAGCTGCGGCGCTGTGTGCTGTACGCGCGCGTGTGAAGAAGTGGCG 480
 DB 118 ATGCAAGAGCTGCGGCGCTGTGTGCTGTACGCGCGCGTGTGAAGAAGTGGCG 177
 QY 481 GTGAACCTGCGGCTGT 540
 DB 178 GTGAACCTGCGGCTGT 237
 QY 541 TGGGCGGTGAACAATGT 600
 DB 238 TGGGCGGTGAACAATGT 257

QY 601 GCGGTGACACAGAGGCTCTCTGTCGCGCGCGCGCTGCGCGACGATCCACT----- 655
 DB 298 GCGGTGACACAGAGGCTCTCTCTGTCGCGCGCGCGCTGCGCGACGATCCACT 357
 QY 656 -----ACCG 705
 DB 358 AACG 417
 QY 706 ATGGCGACGCGGT 765
 DB 418 ATGGCGACCATGT 477
 QY 766 GGTCTCTCTCTGCG 825
 DB 478 GGTCTCTCTGCG 537
 QY 826 ACCCTTCTCTTAACG 885
 DB 538 ACCTTCTCTTAACG 597
 QY 886 GCGGTGATGACTTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 945
 DB 598 GCGGTGATGACTTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 657
 QY 946 ACCGCGCGCTTACTGCGGT 962
 DB 658 ACCGCGCGCTTACTGCGGT 674
 RESULT 7
 ADX52363
 ID ADX52363 standard; cDNA; 1664 BP.
 AC ADX52363;
 XX
 DT 21-APR-2005 (first entry)
 DE plant full length insert polynucleotide seqid 27103.
 XX
 XX plant protectant; plant growth regulant; gene therapy; plant;
 KM cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
 KM extreme osmotic condition; pathogen tolerance; pest tolerance;
 KM growth rate; cell cycle pathway; disease resistance;
 KM galactomanan production; lignin production; plant growth regulator;
 KM yield; plant growth; plant development; seed oil; protein yield;
 KM protein content; gene; ss.
 XX
 OS unidentified.
 OS
 PN US2004034888-A1.
 XX
 PD 19-FEB-2004.
 PF 28-APR-2003; 2003US-00425114.
 PR 06-MAY-1999; 99US-00304517.
 PR 05-NOV-2001; 2001US-00985678.
 XX
 PA (LIU/J) LIU J.
 PA (ZHOU/J) ZHOU Y.
 PA (KOVA/) KOVALIC D K.
 PA (SCRE/) SCREEN S E.
 PA (TABAS/) TABASKA J E.
 PA (CAO/Y) CAO Y.
 PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
 XX
 DR WPI; 2004-180133/17.
 PT New recombinant DNA construct, useful for improving plant tolerance to
 PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
 PT pests, for conferring increased resistance to plant disease, or for

PT improving yield.
XX
XX Claim 1; SEQ ID NO 27103; 15bp; English.
PS
CC The invention describes a recombinant DNA construct comprising a
CC polynucleotide consisting of a sequence encoding an amino acid sequence
CC available in electronic form from the US patent office at
CC ftp://sedate.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
CC of the invention are also useful in physical arrays of molecules and as
CC plant breeding markers. The recombinant DNA construct is useful for
CC improving plant tolerance to cold, heat, drought, herbicides, extreme
CC osmotic conditions, pathogens or pests, for manipulating growth rate in
CC plant cells by modification of the cell cycle pathway, for conferring
CC increased resistance to plant disease, for producing galactonmanan,
CC lignin or plant growth regulators, for increasing the rate of homologous
CC recombination in plants, for improving yield by modification of
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
CC or by providing improved plant growth and development under at least one
CC stress condition or for modifying seed oil or protein yield and/or
CC content. This sequence represents a plant full length insert
CC polynucleotide that can be used in the recombinant DNA construct of the
CC invention.
XX
SQ Sequence 1664 BP; 297 A; 506 C; 489 G; 372 T; 0 U; 0 Other;

```
QY 357 GGTGGCGGACTGCTGAACAAGGGGCAACACGCTGGCACTGTGGCGGCGACGCTGGT 416
DB 134 GGTGGCGGACTGCTGAACAAGGGGCAACACGCTGGCACTGTGGCGGCGACGCTGGT 193
QY 417 GGGGCTGCAAGAGGTGCGGGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 476
DB 194 GGGGCTGCAAGAGGTGCGGGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 253
QY 477 GGGGCTGCAAGAGGTGCGGGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 536
DB 254 GGGGCTGCAAGAGGTGCGGGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 313
QY 537 GGGGCTGCAAGAGGTGCGGGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 596
DB 314 GGGGCTGCAAGAGGTGCGGGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 373
QY 597 GGGGCTGCAAGAGGTGCGGGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 656
DB 374 GGGGCTGCAAGAGGTGCGGGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 433
QY 657 GGGGCTGCAAGAGGTGCGGGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 716
DB 434 GGGGCTGCAAGAGGTGCGGGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 493
QY 717 GGGGCTGCAAGAGGTGCGGGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 776
DB 494 GGGGCTGCAAGAGGTGCGGGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 553
QY 777 GGGGCTGCAAGAGGTGCGGGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 836
DB 554 GGGGCTGCAAGAGGTGCGGGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 613
QY 837 GGGGCTGCAAGAGGTGCGGGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 896
DB 614 GGGGCTGCAAGAGGTGCGGGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 673
QY 897 GGGGCTGCAAGAGGTGCGGGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 956
DB 674 GGGGCTGCAAGAGGTGCGGGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 733
QY 957 GGGGCTGCAAGAGGTGCGGGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 962
DB 734 GGGGCTGCAAGAGGTGCGGGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 739

RESULT 9
AEFI6009 standard; cDNA; 1883 BP.
ID AEFI6009;
AC AEFI6009;
XX
XX 09-MAR-2006 (first entry)
DT
XX
DE Oryza sativa ammonium transporter cDNA SeqID9.
KM ammonium transfer; transgenic plant; nitrogen; cellular transport; gene;
XX ss.
XX
XX Oryza sativa.
OS
XX
XX Key Location/Qualifiers
FH 87.1580
FT CDS /*tag= a
FT /product= "Oryza sativa ammonium transporter"
XX
XX US2006010512-A1.
XX
XX 12-JAN-2006.
XX
XX 15-DEC-2004; 2004US-00012668.
XX
XX 28-DEC-2001; 2001US-00033109.
PR
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XX
PA (ALLEN S. M.
PA (RAFA/ SKI J. A.
XX
XX Allen SM, Rafalski JA;
PI
XX
XX MPI; 2006-088761/09.
DR P-PSDB; AEFI6010.
XX
XX New isolated polynucleotide encoding a polypeptide having ammonium
PT transfer activity, useful for producing transgenic plants with increased
PT nitrogen content.
XX
XX Disclosure; SEQ ID NO 9; 29pp; English.
PS
XX
XX This invention relates to a novel isolated polynucleotide encoding a
CC polypeptide having ammonium transfer activity. The polynucleotides are
CC useful for producing transgenic plants with increased nitrogen content.
CC The present sequence is a cDNA homologous to the sequence of the
CC invention which encodes an ammonium transporter.
XX
XX Sequence 1883 BP; 327 A; 592 C; 607 G; 357 T; 0 U; 0 Other;
SQ
Query Match 10.6%; Score 389.2; DB 15; Length 1883;
Best Local Similarity 74.0%; Pred. No. 8.8e-50;
Matches 493; Conservative 0; Mismatches 173; Indels 0; Gaps 0;
QY 297 GAAGATGCTGCTGCTGCGGACAGGTGTGCGCTGCGCTGACCAAGGAGAACAGTGGCGT 356
DB 74 GAAGATGCTGCTGCTGCGGACAGGTGTGCGCTGCGCTGACCAAGGAGAACAGTGGCGT 133
QY 357 GGTGGCGGACTGCTGAACAAGGGGCAACACGCTGGCACTGTGGCGGCGACGCTGGT 416
DB 134 GGTGGCGGACTGCTGAACAAGGGGCAACACGCTGGCACTGTGGCGGCGACGCTGGT 193
QY 417 GGGGCTGCAAGAGGTGCGGGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 476
DB 194 GGGGCTGCAAGAGGTGCGGGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 253
QY 477 GGGGCTGCAAGAGGTGCGGGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 536
DB 254 GGGGCTGCAAGAGGTGCGGGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 313
QY 537 GGGGCTGCAAGAGGTGCGGGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 596
DB 314 GGGGCTGCAAGAGGTGCGGGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 373
QY 597 GGGGCTGCAAGAGGTGCGGGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 656
DB 374 GGGGCTGCAAGAGGTGCGGGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 433
QY 434 GGGGCTGCAAGAGGTGCGGGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 493
QY 494 GGGGCTGCAAGAGGTGCGGGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 553
DB 554 GGGGCTGCAAGAGGTGCGGGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 613
QY 614 GGGGCTGCAAGAGGTGCGGGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 673
QY 673 GGGGCTGCAAGAGGTGCGGGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 733
DB 733 GGGGCTGCAAGAGGTGCGGGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 739
QY 739 GGGGCTGCAAGAGGTGCGGGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 739
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DB 734 CTGGGT 739

RESULT 10
ADP09621
ID ADP09621 standard; DNA; 401 BP.
XX
AC ADP09621;
XX
DT 26-AUG-2004 (first entry)
XX
DE Rice ammonium transporter DNA with a T-DNA/GUS tag Seqid 12.
XX
KW rice; ammonium transporter; GUS; insertional mutagenesis;
KW beta-glucuronidase; biotic stress resistance; pesticide; herbicide;
KW plant; ds; hygromycin phosphotransferase; HGH; T-DNA; transfer-DNA;
KW chimeric.
XX
OS Oryza sativa.
OS Chimeric.
OS Unidentified.
XX
FH Key Location/Qualifiers
FT misc_feature 1..96
FT /tag= a
FT /note= "T-DNA insert in rice line 1C-109-35"
XX
PN WO2004046357-A1.
XX
PD 03-JUN-2004.
XX
PF 14-NOV-2003; 2003WO-KR002461.
XX
PR 15-NOV-2002; 2002US-0427166P.
XX
PA (POSC-) POSCO.
PA (POST-) POSTECH FOUNDD.
XX
PI An G, Ryu C, Han J, Kang H, An K;
XX
DR WPI; 2004-449751/42.
XX
PT New organ preferential nucleic acids and polypeptides, useful in
PT producing rice plants with desired characteristics and which are
PT resistant to herbicide, plant pathogen, fungi, bacteria, virus, insect,
PT nematode, and stress.
XX
PS Disclosure; SEQ ID NO 12; 296bp; English.
XX
XX This invention relates to a novel method of identifying nucleic acid
XX molecules, or fragments thereof, that are expressed in an organ
XX preferential manner in rice. Specifically, it refers to producing rice
XX cell lines that carry tagged genes modified by T-DNA/GUS based
XX insertional mutagenesis, where the GUS portion of the insert is the
XX promoterless beta-glucuronidase reporter gene that can only be expressed
XX when it is inserted into an active gene. The present invention describes
XX generating transformed rice lines containing transfer-DNA (T-DNA)
XX insertions that also carry a gene encoding the selectable marker
XX hygromycin phosphotransferase (HPT). Accordingly, this method can be used
XX to produce rice plants with desirable characteristics including increased
XX grain yield and nutritional content, resistance to biotic stress,
XX pesticides, herbicides or insects, altered morphology or improved
XX characteristics referring to shape, taste or cooking quality of the
XX grain. This polynucleotide sequence represents the junction region that
XX links a genomic rice gene with a portion of the inserted T-DNA sequence,
XX given in an exemplification of the invention.
XX
SQ Sequence 401 BP; 125 A; 89 C; 68 G; 119 T; 0 U; 0 Other;

Query Match 8.5%; Score 312; DB 12; Length 401;
Best Local Similarity 97.0%; Pred. No. 3..7e-18;
Matches 318; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 2307 TGAGTTTTCTTGTACGACAGCCAGAAAAGCAGCAGTAAATGAAATAGATATTT 2366
DB 74 TGTGTTATTTAACTGTCTAAGCAGCCAGAAAAGCAGCAGTAAATGAAATATTT 133
QY 2367 TTACAGCCTCCCATTTCCGTGGGTGACTTGTCAAAGTCTATTTTACCGCGGAGAGATGA 2426
DB 134 TTACAGCCTCCCATTTCCGTGGGTGACTTGTCAAAGTCTATTTTACCGCGGAGAGATGA 193
QY 2427 CTACAGTACTCATATGCAAAATTTGATGACATACAGGACCTGCTATTCGCAAAAGA 2486
DB 194 CTACAGTACTCATATGCAAAATTTGATGACATACAGGACCTGCTATTCGCAAAAGA 253
QY 2487 TCCGTGCTCTTATTTATGACACATGACACACCTACACCCCTTATCATTTATTTGTTT 2546
DB 254 TCCGTGCTCTTATTTATGACACATGACACACCTACACCCCTTATCATTTATTTGTTT 313
QY 2547 TTAGATTTGTGGTATTAATATACAGATTTCAATATGACATTAATGATTTTCTTTTCC 2606
DB 314 TTAGATTTGTGGTATTAATATGAGATTTCAATATGACATTAATGATTTTCTTTTCC 373
QY 2607 GTACACACACGAAATCTCATTAATAT 2634
DB 374 GTACACACACGAAATCTCATTAATATAT 401

RESULT 11
AAL53989
ID AAL53989 standard; cDNA; 1961 BP.
XX
AC AAL53989;
XX
DT 18-FEB-2003 (first entry)
XX
DE cDNA encoding a soybean high affinity ammonium transporter protein #2.
XX
KW Herbicide; ammonium transporter protein; herbicide; transgenic plant;
KW soybean; gene; ss.
XX
OS Glycine max.
XX
FH Key Location/Qualifiers
FT CDS 214..1674
FT /*tag= a
FT /product= "Soybean high affinity ammonium transporter
FT protein"
XX
PN US2002142390-A1.
XX
PD 03-OCT-2002.
XX
PF 28-DEC-2001; 2001US-00033109.
XX
PR 28-AUG-1998; 98US-0098248P.
PR 27-AUG-1999; 99US-00384625.
XX
PA (ALIE/) ALLEN S M.
PA (RAFA/) RAFALSKI J A.
XX
PI Allen SM, Rafalski JA;
XX
DR WPI; 2003-102520/09.
DR P-PSDB; AAO26537.
XX
PT Novel ammonium transporter polypeptide useful for identifying enzymatic
PT inhibitors, which is homologous to corn, soybean, wheat or rice ammonium
PT transporter polypeptides.
XX
PS Claim 3; Page 21-22; 27pp; English.
XX
XX The invention relates to a novel ammonium transporter protein comprising
XX 90% homology based on the Clustal method compared to: a corn ammonium
XX transporter polypeptide of 183 or 63 amino acids; a soybean ammonium
XX transporter polypeptide of 500 or 486 amino acids; a wheat ammonium

CC transporter polypeptide of 494 or 470 amino acids; and a rice ammonium
CC transporter 497 amino acids fully defined in the specification. The
CC isolated polynucleotide is useful for selecting an isolated
CC polynucleotide that affects the level of expression of the ammonium
CC transporter polypeptide in a plant cell. The ammonium transporter protein
CC is useful for preparing antibodies which are useful for detecting the
CC transporter protein in situ in cells or in vitro in cell extracts, and as
CC targets to facilitate design and/or identify inhibitors of the enzymes
CC that are useful as herbicides. The isolated polynucleotide is also useful
CC for creating transgenic plants in which the polynucleotide is present at
CC higher or lower levels than normal, and for designing and producing
CC primer pairs which are useful in amplification or primer extension
CC reactions. This polynucleotide sequence represents the cDNA encoding a
CC soybean high affinity ammonium transporter protein of the invention
XX
SQ Sequence 1961 BP; 490 A; 407 C; 472 G; 592 T; 0 U; 0 Other;
Query Match 7.9%; Score 289.6; DB 8; Length 1961;
Best Local Similarity 67.0%; Pred. No. 1.2e-34;
Matches 409; Conservative 0; Mismatches 201; Indels 0; Gaps 0;
QY 353 CGTCGTCGCGGAGCTGCTGACCAAGGAGGAGCAAGCGGTCGAGCTGCTGCGGCGAGCGC 412
DB 248 CGCGCGACCCGAAATGCTGAACAAAGGTGACAAAGCATGCGCTAAACAGCAGCCACC 307
QY 413 TGGTGGGCTGCGAGCGCTCCGCGCTTGGTGTCTGCTGACGCGCGCTGTGAAGA 472
DB 308 TCGTGGCTCTTCAAGAGCATCCGCGCTCTCTGATCTCTACGCGCATGTGAAGAAA 367
QY 473 AGTGGGCGGGAACCTGCGCGCTTACAGCGCTTACGCGCTTGGAGTCTGCT 532
DB 368 AATGGGAGGAACTGAGCTTTCATGAGCTCTACGCGCTTGGCGCGCTTCTAATGTT 427
QY 533 GGGTCACTGGGCGTACCAACATGCTTCCGGGAGAGCTCTCCGATTCGGGAGAG 592
DB 428 GGGTGTGTGTGTACCGAATGCGCTTGGAGAGAACTTTCCCTTGGGAGAAAG 487
QY 593 CGCGCGCGGCGCTGAGCAGAGGCTCTGCTGCGCGCGCGCGCTGCGCGAGCTCC 652
DB 488 GTGCTCAGACCTAGGCGCAAGTCTCTCAAGAAAGCATATGATTAAGCAATCC 547
QY 653 ACTACCGCGCGGAGCGGAGGAGAGCGGCGCGGCTGACCGATGGCGA 712
DB 548 ACCACTTGTATATGAGCATGTGATACCTCTGAGAACTTTTACCTATGGCTT 607
QY 713 CGGTGTGTACTTCAAGTGTGCTGCGCGCATACCTTCATCTGTCGCGGCTCCC 772
DB 608 CGCTGTGTATTTCCATTTCACTTTGCTGTATTACTTTTGTGGCTGCTG 667
QY 773 TCTCGGCGGATGAGCTTCTCGCTGTGATGATCTTCCGCTGCTCACTTCT 832
DB 668 TCTTGGCCGAAATGACATCAAGGCTTGAAGCTTTTGTGCTTTGATCTTTT 727
QY 833 CCAACCGCGCGGCTTCTCTCTGCGCGCGGCTTCTCTTCACTGGGCGTCA 892
DB 728 CCAACAGTGGCGCTTGAATGCTTGTGGGAGTGGCTTCTTCACTAAGGAGGCTTA 787
QY 893 TCGACTACTGCGCGGCTGATCACTCACTCCGCGGATGCGCGGCTTCACTCCG 952
DB 788 TTGATATATTTGCGCGGCTATGATACACTTTCTTGTGAATGCGCTTCACTGCTG 847
QY 953 CTTACTGGGT 962
DB 848 CTTACTGGGT 857
RESULT 12
AEF16011
ID AEF16011 standard; cDNA; 1961 BP.
XX AEF16011;
AC AEF16011;
XX
DT 09-MAR-2006 (first entry)

XX
DE Glycine max ammonium transporter cDNA SeqID11.
XX
KW ammonium transfer; transgenic plant; nitrogen; cellular transport; gene;
XX ss.
XX
OS Glycine max.
XX
FH Key Location/Qualifiers
FT CDS 214..1674
FT /tag= a
FT /product= "Glycine max ammonium transporter"
XX
PN US2006010512-A1.
XX
PD 12-JAN-2006.
XX
PF 15-DEC-2004; 2004US-00012668.
XX
PR 28-DEC-2001; 2001US-00033109.
XX
PA (ALBE/) ALLEN S M.
XX PA (RAFA/) RAFALSKI J A.
XX
PI Allen SM, Rafalski JA;
XX WPI; 2006-088761/09.
XX P-PDB; AEF16012.
XX
PT New isolated polynucleotide encoding a polypeptide having ammonium
PT transfer activity, useful for producing transgenic plants with increased
PT nitrogen content.
XX
PS Disclosure; SEQ ID NO 11; 29pp; English.
XX
CC This invention relates to a novel isolated polynucleotide encoding a
CC polypeptide having ammonium transfer activity. The polynucleotides are
CC useful for producing transgenic plants with increased nitrogen content.
CC The present sequence is a cDNA homologous to the sequence of the
CC invention which encodes an ammonium transporter.
XX
SQ Sequence 1961 BP; 490 A; 407 C; 472 G; 592 T; 0 U; 0 Other;
Query Match 7.9%; Score 289.6; DB 15; Length 1961;
Best Local Similarity 67.0%; Pred. No. 1.2e-34;
Matches 409; Conservative 0; Mismatches 201; Indels 0; Gaps 0;
QY 353 CGTCGTCGCGGAGCTGCTGACCAAGGAGGAGCAAGCGGTCGAGCTGCTGCGGCGAGCGC 412
DB 248 CGCGCGACCCGAAATGCTGAACAAAGGTGACAAAGCATGCGCTAAACAGCAGCCACC 307
QY 413 TGGTGGGCTGCGAGCGCTCCGCGCTTGGTGTCTGCTGACGCGCGCTGTGAAGA 472
DB 308 TCGTGGCTCTTCAAGAGCATCCGCGCTCTCTGATCTCTACGCGCATGTGAAGAAA 367
QY 473 AGTGGGCGGTAAGTGGGCTTCAATGCGCTCTACGCGCTTCCGCGCGCTGTGATCTGCT 532
DB 368 AATGGGCAATGAACTGAGCTTTCATGAGCTCTACGCGCTTGGGCGGCTTCTAATGTT 427
QY 533 GGGTCACTGGGCGTACCAACATGCTTCCGGGAGAGCTCTCCGATTCGGGAGAG 592
DB 428 GGGTGTGTGTGTACCGAATGCGCTTGGAGAGAACTTTCCCTTGGGAGAAAG 487
QY 593 CGCGCGCGGCGCTGAGCAAGGAGCTCTGTCGCGCGCGCGCTGCGCGAGCGTCC 652
DB 488 GTGCTCAGACCTAGGCGCAAGTCTCTCAGCAAGAAAGCATATGATTAAGCAATCC 547
QY 653 ACTACCGCGCGGAGCGGAGGAGAGCGGCGGCTGAGCGCGCTGTACCGGATGGCGA 712
DB 548 ACCACTTGTATATGAGCATGTGATACCTCTGAGAACTTTTACCTATGGCTT 607
QY 713 CGGTGTGTACTTCAAGTGTGCTGCGCGCATACCTTCATCTGTCGCGGCTCCC 772

Db 608 CGCTGTGATATTCGAATTCACATTTTGTGCTATTAATCTATATTGTGCGGCTCG 667
QY 773 TCCTGGCGCCGATGAGCTTCTCGCTGATGATCTTGTCCGCTCTGACCTTCT 832
Db 668 TCCTTGGCCGAATGAACTCAAGGCTTGATGCTTTGTGCTCTTGTGATCTTT 727
QY 833 CCTACACGCTGCGGCTTCTCTCTGCGGCGGCGGCTTCTCTCACTGAGGCGTCA 892
Db 728 CCTACACAGTCCGGGCTTTTAACTTTGGGGTGTGTGCTTTCTTACCAATGGGCGTTA 787
QY 893 TCGACTACTGCGCGGCTACGTCATCAGCTCTCGCGCGCATCGCGGCTTACCGCG 952
Db 788 TTGATATATTCTGCGGCTATGTCATACACTTCTTCTGGAATCGCTGCTTACCTGCTG 847
QY 953 CTTACTGGGT 962
Db 848 CTTACTGGGT 857

RESULT 13

ACL28017
ID ACL28017 standard; cDNA; 977 BP.AC 28017;
XX
XXDT 02-JUN-2005 (first entry)
XX
XXDE Rice abiotic stress responsive polynucleotide SEQ ID NO:1973.
XX
XXKW ss; abiotic stress tolerance; transgenic plant; plant; cereal;
XX
XXKW agriculture.
XX
XXOS Oryza sativa.
XX
XXPN WO2003008540-A2.
XX
XXPD 30-JAN-2003.
XX
XXPP 21-JUN-2002; 2002WO-US019668.
XX
XXPR 22-JUN-2001; 2001US-0300112P.
XX
XXPR 24-AUG-2001; 2001US-0314662P.
XX
XXPR 26-SEP-2001; 2001US-0325277P.
XX
XXPR 21-NOV-2001; 2001US-0332132P.
XX
XX(SYGN) SYNGENTA PARTICIPATIONS AG.
XX
XXPI Krepis J, Briggs SP, Cooper B, Glazebrook J, Goff SA, Katagiri F,
XX
XXPI Moughamer T, Provart N, Rieke D, Zhu T;
XX
XXWPI; 2003-248011/24.
XX
XXPS Claim 1; SEQ ID NO 1973; 89pp; English.
XX
XX

XX The invention relates to novel abiotic stress responsive polynucleotides
XX and polypeptides. Also disclosed are vectors, expression cassettes, host
XX cells, and plants containing such polynucleotides. Also disclosed are
XX methods for using the polynucleotides and polypeptides to alter the
XX responsiveness of a plant to abiotic stress. The invention is useful in
XX agriculture. The nucleic acid is useful for determining whether a test
XX plant has been exposed to an abiotic stress condition. It is also useful
XX for selecting an agent that alters abiotic stress regulated
XX polynucleotide expression in a plant cell, and to identify a homolog or
XX ortholog to an abiotic stress responsive polynucleotide. The nucleic acid
XX molecule and the polypeptide encoded by it are useful in altering the
XX responsiveness of a plant to an abiotic stress, such as cold stress, salt
XX stress, osmotic stress or any of their combinations. The present sequence
XX is used in the exemplification of the invention

SQ Sequence 977 BP; 131 A; 333 C; 330 G; 181 T; 0 U; 2 Other;

Query Match 7 6%; Score 279.6; DB 11; Length 977;
Beet Local Similarity 78.3%; Pred. No. 3.5e-33;
Matches 349; Conservative 0; Mismatches 94; Indels 3; Gaps 1;

QY 2880 GCAGGGGTGTGTCAGAGGGGTGGCGCGCTGTGTATGAGGGGTGCTTCGCGGAGCATCCG 2939

Db 508 GCAGGCTGTGTGTCAGACGTTGGCGCGGCTACTGATGGGCATCTGTGGGCGAGCTGGCG 567

QY 2940 TGTATACCATGATGATCTTCCACAGCGCTTCAGAACTCTTCAGACGCGTGCAGACACC 2999

Db 568 TGGTCTCCATGATGATCTTCCACAGAGATCGGCGCTTCAGAAAGTGGACGACACC 627

QY 3000 CTGGGCGCTTCCACACCGCGGTGCGCGGCTCTCGGCGGCTCTGACCGGCGCTC 3059

Db 628 CTGGCGCTTCTTCACACCGCGCGGTGCGGCGCTCTCTGCGGCGCTCTTCCACGGGCGCTG 687

QY 3060 TTGCGCGAGCCGACCCCTCTGCAACCTCTTCTCTCCGCTGCGGCGACTCCCGGCGCGCTTC 3119

Db 688 TTGCGCTTTCGCGGACCTTCACCGCGCTTCACACCGCATCCGCGGCGCGCGCGCTTC 747

QY 3120 TAGGCTTC 3179

Db 748 TACGCGCG---CGGATCGCGCGCGGGAAGCAGATCGCGCGCGCGCGCGCTTCCTGCTC 804

QY 3180 GCGTGGAAAGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3239

Db 805 GTGTGGAAAGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 864

QY 3240 CGCATGCCCGGCT 3299

Db 865 CGCATGCCCGGCT 924

QY 3300 GCGCTCTGGGCT 3325

Db 925 GCGCTATGGGAGAGCT 950

RESULT 14

ADX3169
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XX
XXDT 21-APR-2005 (first entry)
XX
XXDE Plant full length insert polynucleotide seqid 14489.
XX
XXKW plant protectant; plant growth regulant; gene therapy; plant;
XX
XXKW recombinant DNA construct; physical array; plant breeding marker;
XX
XXKW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
XX
XXKW extreme osmotic condition; pathogen tolerance; pest tolerance;
XX
XXKW growth rate; cell cycle pathway; disease resistance;
XX
XXKW galactomanan production; lignin production; plant growth regulator;
XX
XXKW yield; plant growth; plant development; seed oil; protein yield;
XX
XXOS Unidentified.
XX
XXPN US2004034888-A1.
XX
XXPD 19-FEB-2004.
XX
XXPF 28-APR-2003; 2003US-00425114.
XX
XXPR 06-MAY-1999; 99US-00304517.
XX
XXPR 05-NOV-2001; 2001US-00985678.
XX
XXPA (LITU/) LITU J.
XX
XXPA (ZHOU/) ZHOU Y.
XX
XXPA (KOVA/) KOVALIC D K.
XX
XXPA (SCRE/) SCREEN S E.
XX
XX

Best Local Similarity 71.1%; Pred. No. 2,1e-28;
Matches 328; Conservative 0; Mismatches 133; Indels 0; Gaps 0;

```
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      153 AGGCGTGGTGCAAGGGGTGGGAGCCATTTGTCAATGGGAATTTCTCAGTAGCATCCCCTG 212
QY      2942 GTACACATGATGATCTCTCCACAAGGCTCCAAAGATCTTGCAAGCGGTGAGACACCTT 3001
      213 GTACACTATGATGTACTGCACAAGAAATGTCTTTCATGCAAGAGATGACGACACCTT 272
QY      3002 CGGCGTCTTCCACACACCCACGCGGTGCGCGGCTCTCTCGGGGCTCTCTCACCGGCTCTT 3061
      273 CGGCGTATTCACACCCATGCGGTGCGGTGCGGTCTCTCGGGGCTCTCTCACGACTCTT 332
Db      3062 CGCCGAGCCACCTCTGTGAACCTCTTCTCCCGTGGCCGACTCCGGGGCGCTTCTTA 3121
      333 TGCTGAGCTGTCTCTGTGCAACCTTCTCTGCGCATCCGGACTCCAGAGTGCAATTTTA 392
QY      3122 CGGCGGCGCGGCGGCGGCCCATGTTGGGCAAGATGCGCGGCGGCTCTTGTGTGCGC 3181
      393 TGTGTGTGATGTGTGATCAAGTTTGGGAAGCAGATGCTGGGCGCACTCTTGTCATTGG 452
QY      3182 CTGGAACTGTGTGTGATCTCCCTCATCTGCTCGGCATCAACCTCTGTCGCGCTCCG 3241
      453 CTGGAACTTTTATCATCTTCATATCTGTGTCTTATTTGGGCTAGTCTGCCCCCTCG 512
QY      3242 CATGCCGACGACAGAGCTGAGGTGCGGCGACGAGCGGCTCCAGCGGAGAGGCTTACGC 3301
      513 AATTCTGTATGCACAGCTCTTATCGGGGATGATGCTGTACATGTGTAGAGGAGCGTATGC 572
QY      3302 GCTCTGGGGCGACGGGGAGATGTACAGCTCAACCAAGCAAG 3342
      573 TATATGGGCAAGAGCGAGCTCAACGATGTAACTCCGCAAG 613
Db
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Search completed: July 23, 2006, 20:00:02
Job time : 2153 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 23, 2006, 20:00:17 ; Search time 16351 Seconds
(without alignments)
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Scoring table: IDENTITY NUC
Gapop 10_0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

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Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: gb_esc5:*
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12: gb_esc13:*
13: gb_esc14:*
14: gb_esc15:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	643.6	17.5	700	5	C1146333 C1146333
2	642.6	17.5	700	5	C1135879 C1135879
3	631	17.2	639	5	CK077340 85263rslc
4	630.2	17.1	647	13	CL795215 OR CBA000
5	604	16.4	650	5	C1138721 C1138721
6	557.8	15.2	599	5	C1146832 C1146832
7	556.4	15.1	650	5	C1145244 C1145244
8	554	15.1	600	5	C1275500 C1275500
9	551.8	15.0	639	5	C1277861 C1277861
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11	531.4	14.5	589	4	CB678450 OSJNE16H
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15	497.8	13.5	685	14	DX307908 OR ABA021
16	496	13.5	534	4	C1134465 C1134465
17	493	13.4	877	8	CO460978 MZCCL1503
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27	454	12.3	500	5	C1179514
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32	439.8	12.0	673	4	CA141237
33	423.8	11.5	800	14	DUI592899
34	422.4	11.5	471	5	CI355059
35	420	11.4	707	13	CW168467
36	419	11.4	770	10	DV522315
37	418.8	11.4	734	13	CW405591
38	411	11.2	640	4	CA191252
39	405.6	11.0	450	5	CI177804
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42	400.6	10.9	685	10	DR790051
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44	398.6	10.8	742	12	CC607787
45	394	10.7	708	12	CL151156

ALIGNMENTS

RESULT 1
LOCUS C1146333
DEFINITION C1146333 Oryza sativa (japonica cultivar-group) mixed shoot
(Normalized library) Oryza sativa (japonica cultivar-group) cDNA
clone 028-W081R-G03 3', mRNA sequence.
C1146333 700 bp mRNA linear EST 05-FRB-2006
C1146333.1 GI:86503700
C1146333
VERSION
KEYWORDS
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Bukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BPP
clade; Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 700)
Kikuchi, S.
Collection and mapping of over 30,000 transcription units by the
rice full-length cDNA project from japonica rice
Unpublished (2006)
Contact: Shoshi Kikuchi
Department of Molecular Genetics, Head of Laboratory of Gene
Expression
National Institute of Agrobiological Sciences
2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan
Tel: 81-29-838-7007
Fax: 81-29-838-7007
Email: skikuchi@ias.affrc.go.jp
This EST clone is one of 780K ESTs of Rice full length cDNA Project
URL: http://cdna01.dna.affrc.go.jp/cdna/
NIAS Rice Full-length cDNA Project Team: Kikuchi, S., Satoh, K.,
Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yezaki, J.,
Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T.,
Ohneda, E., Yanagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T.,
Yamamoto, M., and Nakahama, Y.
FAIS Genome Sequencing & Analysis Group: Ootomo, Y., Iida, Y.,
Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M.,
Kodama, T., Kurosaki, T., Kusumegi, T., Lu, M., Masuda, H., Miura, J.,
Mizuno, K., Natikawa, R., Nikiura, J., Oka, M., Ryu, R., Sugano, S.,
Yoshimura, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S.,
Yoshimura, A., Matubara, K., and Murakami, K.
Genome Exploration Research Group in Riken Genomic Sciences Center
and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K.,

Akimura,T., Arawaka,T., Carninci,P., Fukuda,S., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hirooka,T., Hori,F., Iida,J., Imamura,K., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kanagawa,S., Katoh,H., Kawai,J., Kishikawa-Hirozane,T., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koyu,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Ohno,M., Otsu,N., Ota,Y., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Sato,K., Shibata,K., Shingawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagami-Takeda,Y., Tagawa,A., Takahashi,F., Takeku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Waki,K., Yasunishi,A. and Hayashizaki,Y.

FEATURES

source

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ORIGIN

Query Match 17.5%; Score 643.6; DB 5; Length 700;
Best Local Similarity 97.6%; Pred. No. 5.2e-116;
Matches 687; Conservative 0; Mismatches 9; Indels 8; Gaps 3;

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3078 TCACAACCT 3137
121 TCACAACCT 180
3138 GCCCACTTGGGAGAGAGATCGCGCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3197
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3198 ACTCCCTCATCTGCGCTCGCATCAACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3257
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301 CTCGAGGTGCGGAGACGCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 360
3318 GAGATGATAGAGTCTACCAAGCAGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3377
361 GAGATGATAGAGTCTACCAAGCAGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 420
3378 TCGATCACAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3437
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3438 AGAAATTAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3497
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537 TACGATGATTAACAGCGCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 596
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3614 CTGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3657

Db 657 CTGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 700

RESULT 2
C1135879
LOCUS
DEFINITION
C1135879 Oryza sativa (japonica cultivar-group) mixed callus
(Normalized Library) Oryza sativa (japonica cultivar-group) cDNA
clone 027-M018R-A04 3', mRNA sequence.

ACCESSION
C1135879.1 GI:86493246

VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Bp
clade; Ehrhartoideae; Oryzoae; Oryza.

REFERENCE
AUTHORS
TITLE
Kikuchi,S.
Collection and mapping of over 30,000 transcription units by the
rice full-length cDNA project from japonica rice
Unpublished (2006)
Contact: Shoshi Kikuchi
Department of Molecular Genetics, Head of Laboratory of Gene
Expression
National Institute of Agricultural Sciences
2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan
Tel: 81-29-838-7007
Fax: 81-29-838-7007
Email: skikuchi@niae.affrc.go.jp
URL: http://cdna01.dna.affrc.go.jp/cDNA/
This EST clone is one of 780k ESTs of Rice full length cDNA Project

JOURNAL
COMMENT

NIAS Rice Full-length cDNA Project Team: Kikuchi,S., Sato,K., Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,T., Ishikawa,M., Yamada,H., Ooka,H., Hotta,T., Kojima,K., Namiki,T., Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Oheauki,K., Shishiki,T., Yamamoto,M. and Nakahama,Y.
FAIS Genome Sequencing & Analysis Group: Otsu,Y., Iida,Y., Fujimura,T., Ikeda,R., Ishibiki,J., Kawamata,M., Kobayashi,M., Kodama,T., Kurosaki,T., Kusumegi,T., Lu,M., Maeda,H., Miura,J., Mizuno,K., Naitakawa,R., Naitakawa,R., Oka,M., Ryu,R., Sugano,S., Sugiyama,A., Suzuki,Y., Tsunoda,Y., Ueda,M., Xie,Q., Yokomizo,S., Yoshimura,A., Matsubara,K. and Murakami,K.
Genome Exploration Research Group in Riken
and Genome Science Laboratory in Riken: Adachi,J., Aizawa,K., Akimura,T., Arawaka,T., Carninci,P., Fukuda,S., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hirooka,T., Hori,F., Iida,J., Imamura,K., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kanagawa,S., Katoh,H., Kawai,J., Kishikawa-Hirozane,T., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koyu,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Ohno,M., Otsu,N., Ota,Y., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Sato,K., Shibata,K., Shingawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagami-Takeda,Y., Tagawa,A., Takahashi,F., Takeku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Waki,K., Yasunishi,A. and Hayashizaki,Y.

FEATURES

source

1. 700
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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/db_xref="taxon:39947"
/clone="027-M018R-A04"
/tissue_type="mixed callus (Normalized Library)"
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ORIGIN

Query Match 17.5%; Score 642.6; DB 5; Length 700;
Best Local Similarity 97.6%; Pred. No. 8.2e-116;
Matches 686; Conservative 0; Mismatches 9; Indels 8; Gaps 3;

QY 2957 CCTCCACAAGCGCTCAAGATCTCTGAGCGCTGACGACACCTCGGCGTCTTCCACAC 3016
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 QY 3017 CCAGCGCTCGCGCGCTCTCTGAGCGCTCTCTCAACCGGCTCTTCCGAGCCCACTT 3076
 DB 61 CCAGCGCTCGCGCGCTCTCTGAGCGCTCTCTCAACCGGCTCTTCCGAGCCCACTT 120
 QY 3077 CTGCAACCT 3136
 DB 121 CTGCAACCT 180
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 DB 181 CGCCGAGTTCGCGCAAGATCGCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
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 DB 241 CACCTTCCT 300
 QY 3257 GCTCGAGTTCGCGCAAGATCGCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3316
 DB 301 GCTCGAGTTCGCGCAAGATCGCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 360
 QY 3317 CGAGATGTACGAGCTGACCAAGACAGCTCTCGACCGCGCTGCGCCCGCTGCTGATG 3376
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 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BPP
 clade; Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 639)
 Yu, J., Wang, J., Lin, W., Li, S., Li, H., Zhou, J., Ni, P., Dong, W.,
 Hu, S., Zeng, C., Zhang, J., Zhang, Y., Li, R., Xu, Z., Li, S., Li, X.,
 Zheng, H., Cong, L., Lin, L., Yin, J., Geng, J., Li, G., Shi, J., Liu, J.,
 Lv, H., Li, J., Deng, J., Ran, L., Shi, X., Wang, X., Wu, Q.,
 Li, C., Ren, Y., Wang, J., Wang, X., Li, D., Liu, D., Zhang, X., Ji, Z.,
 Zhao, W., Sun, Y., Zhang, Z., Bao, J., Han, Y., Dong, L., Ji, J., Chen, P.,
 Wu, S., and Liu, J.
 The Genomes of Oryza sativa: A History of Duplications

JOURNAL PLOS Biol. 3 (2), e38 (2005)
 PUBMED 15685292
 COMMENT Contact: Yan Zhou
 Bioinformatics Department
 Hangzhou Genomics Institute
 No. 51 Zhijiang Road, Hangzhou 310008, China
 Tel: 86-571-56805886
 Fax: 86-571-56805884
 Email: zhouyan@genomics.org.cn
 Seq primer: M13 Forward
 High quality sequence stop: 639
 POLYA=No.
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 /mol_type="mRNA"
 /cultivar="LYP9"
 /db_xref="taxon:39946"
 /tissue_type="whole plant"
 /dev_stage="booting"
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 library"
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 Best Local Similarity 100.0%; Pred. No. 1.6e-113; Indels 0; Gaps 0;
 Matches 631; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 271 ACCTTAGTGTGTGTAATTCAGCAGCAAGATGCTGCTCGCGACAGGTGTGCGCTG 330
 DB 9 ACCTTAGTGTGTGTAATTCAGCAGCAAGATGCTGCTCGCGACAGGTGTGCGCGCTG 68
 QY 331 GCGTACAGAGGAGACAGTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 390
 DB 69 GCGTACAGAGGAGACAGTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 128
 QY 391 TGGCAGCTGTGCGCGCGACAGTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 450
 DB 129 TGGCAGCTGTGCGCGCGACAGTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 188
 QY 451 TACGCGCGCGGTGTAAGAAAGTGGCGGTGAACTCGCGCTGTAATGCGGCTGTAAGCC 510
 DB 189 TACGCGCGCGGTGTAAGAAAGTGGCGGTGAACTCGCGCTGTAATGCGGCTGTAAGCC 248
 QY 511 TTGCGCGCGGTGTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 570
 DB 249 TTGCGCGCGGTGTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 308
 QY 571 CTCCTCCGATCTGGGAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 630
 DB 309 CTCCTCCGATCTGGGAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 368
 QY 631 GCCGCGCTGCGCGCGACAGTCTCACTACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 690
 DB 369 GCCGCGCTGCGCGCGACAGTCTCACTACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 428
 QY 691 GAGCGCGTGTACCGATGCGAGCGGTGTGTAATCTTCACTGCGGTGTGCGCGCGCGCG 750
 DB 429 GAGCGCGTGTACCGATGCGAGCGGTGTGTAATCTTCACTGCGGTGTGCGCGCGCGCG 488
 QY 751 CTCATCTCTGTGCGCGCGCT 810
 DB 489 CTCATCTCTGTGCGCGCGCT 548
 QY 811 GTCCGCGCTGCGCTCACTCTCTCAACCGTGGCGCTTCTCTCTCTCTCTCTCTCTCTCTCT 870
 DB 549 GTCCGCGCTGCGCTCACTCTCTCAACCGTGGCGCTTCTCTCTCTCTCTCTCTCTCTCTCT 608
 QY 871 TTCTCTTCTCACTGGGCGCTCATCACTACT 901
 DB 609 TTCTCTTCTCACTGGGCGCTCATCACTACT 639

RESULT 4
 CL795215 647 bp DNA linear GSS 06-AUG-2004
 LOCUS OR_CBa0004P07.r OR_CBa Oryza rufipogon genomic clone OR_CBa0004P07
 DEFINITION 3', genomic survey sequence.
 ACCESSION CL795215
 VERSION CL795215.1 GI:51017231
 KEYWORDS GSS.
 SOURCE Oryza rufipogon
 ORGANISM Oryza rufipogon
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BGP
 clade; Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 647)
 Kim,H., Yu,Y., Mabsotaki,M., Yost,D., Stum,D., Rao,K., Luo,M.,
 Jettly,R., Kudrna,D., Muller,C., Hatfield,J., Soderlund,C. and
 Wing,R.
 TITLE OMAP project
 JOURNAL Unpublished (2004)
 COMMENT Contact: Rod A. Wing
 Arizona Genomics Institute
 University of Arizona
 Forbes Building Room 303, Tucson, AZ 85721-0036, USA
 Tel: 520 626 9595
 Fax: 520 621 1259
 Email: rwing@genome.arizona.edu
 PCR PRIMERS
 FORWARD: TGA TAC GAC TCA CTA TCG GG
 BACKWARD: CAC TCA TTA GGC ACC CCA
 Plate: 0004 row: P column: 07
 Seq primer: CAC TCA TTA GGC ACC CCA
 Class: BAC ends.
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 dk treated 36 hrs before harvest"

ORIGIN
 Query Match 17.1%; Score 630.2; DB 13; Length 647;
 Best Local Similarity 99.4%; Pred.No.2,3e-113;
 Matches 643; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

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 |||||||
 DB 1 AGTGTGTGTGAATCGGCACAAAGTGTCTGTCTGGGACGCTGCTGCGCTGCGCTA 60
 |||||||
 OY 336 CCAGGGGAACACAGTCGCGCTGCGCTGCGGACTGTGAACAAGGGGGAACAAGCGCTGCGA 395
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 DB 61 CCAGGGGAACACAGTCGCGCTGCGCTGCGGACTGTGAACAAGGGGGAACAAGCGCTGCGA 120
 |||||||
 OY 366 GCTGTGTGGCGGACGCTGTGTGGGCTGCAAGACGCTGCGGCGCTGTGTGTGTGTA 455
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 DB 121 GCTGTGTGGCGGACGCTGTGTGGGCTGCAAGACGCTGCGGCGCTGTGTGTGTGTA 180
 |||||||
 OY 456 CGGCGGTGAAGAAGATGGGCGGTGAACCTCGGCGTTCAATGGGCTCTAGCGCTTGGC 515
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 DB 181 CGGCGGTGAAGAAGATGGGCGGTGAACCTCGGCGTTCAATGGGCGCTCTAGCGCTTGGC 240
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 OY 516 CGCGGTGTGTGATCTGTGTGGGTACCTGTGGCGTGAACAATGTCTGTGGGGAAGCTCT 575
 |||||||
 DB 241 CGCGGTGTGTGATCTGTGTGGGTACCTGTGGCGTGAACAATGTCTGTGGGGAAGCTCT 300
 |||||||
 OY 576 CCCGATCTGGGGGAAGGCGCGCGCGCTGTGAACAAGGCGCTTCTCTGTGTGGCGCGCGCG 635
 |||||||
 DB 301 CCCGATCTGGGGGAAGGCGCGCGCGCTGTGAACAAGGCGCTTCTCTGTGTGGCGCGCGCG 360
 |||||||

OY 636 GCTGCCGGGACCGGTCCTACCTACCGGCGGACGAGCGGTGAGACGCGGGGTTGAGACC 695
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 DB 361 GCTGCCGGGACCGGTCCTACCTACCGGCGGACGAGCGGTGAGACGCGGGGTTGAGACC 420
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 OY 696 GCTGTACCCGATGAGGACGAGCGGTGTGTACTTCCAGTGCCTTTTGTGGCGGCATCACCTTCAT 755
 |||||||
 DB 421 GCTGTACCCGATGAGGACGAGCGGTGTGTACTTCCAGTGCCTTTTGTGGCGGCATCACCTTCAT 480
 |||||||
 OY 756 CCTGTGCGCGGCT 815
 |||||||
 DB 481 CCTGTGCGCGGCT 540
 |||||||
 OY 816 GCTGTGCGGTCACCTTCT 875
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 DB 541 GCTGTGCGGTCACCTTCT 600
 |||||||
 OY 876 CTTCCACTGGGGCGCTCA-TCGACTACTGCGGCGGCTAGCTATCCAC 921
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 DB 601 CTTCCACTGGGGCGCTCACTCGACTACTGCGGCGGCTAGCTATCCAC 647
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RESULT 5
 C1138721 650 bp mRNA linear EST 05-FEB-2006
 LOCUS C1138721
 DEFINITION C1138721 Oryza sativa (japonica cultivar-group) mixed callus
 (Normalized library) Oryza sativa (japonica cultivar-group) cDNA
 clone 027-M076R-H04 3', mRNA sequence.
 C1138721
 C1138721.1 GI:86496088
 EST.
 Oryza sativa (japonica cultivar-group)
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BGP
 clade; Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 650)
 Kikuchi,S.
 Collection and mapping of over 30,000 transcritpion units by the
 rice full-length cDNA project from japonica rice
 Unpublished (2006)
 Contact: Shoshi Kikuchi
 Department of Molecular Genetics, Head of Laboratory of Gene
 Expression
 National Institute of Agrobiological Sciences
 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan
 Tel: 81-29-838-7007
 Fax: 81-29-838-7007
 Email: skikuchi@niae.affrc.go.jp
 This EST clone is one of 780k ESTs of Rice full length cDNA Project
 URL: <http://cdna01.dna.affrc.go.jp/cDNA/>
 NIAS Rice Full-length cDNA Project Team: Kikuchi,S., Satoh,K.,
 Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J.,
 Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Naniki,T.,
 Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohsuuki,K., Shieniki,T.,
 Yamamoto,M. and Nakahama,Y.
 PAIS Genome Sequencing & Analysis Group: Osono,Y., Iida,Y.,
 Fujimura,T., Ikeda,R., Ishibiki,J., Kawamata,M., Kobayashi,M.,
 Kodama,T., Kurotaki,T., Kusumegi,T., Lu,M., Maeda,H., Miura,J.,
 Mizuno,K., Naitaka,R., Naitaka,R., Naitaka,R., Naitaka,R.,
 Sugiyama,K., Suzuki,Y., Teunoda,Y., Ueda,M., Xie,Q., Yokomizo,S.,
 Yoshimura,A., Matsubara,K. and Murakami,K.
 Genome Exploration Research Group in Riken Genomic Sciences Center
 and Genome Science Laboratory in Riken: Adachi,J., Aizawa,K.,
 Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hanagaki,T.,
 Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K.,
 Hiraoka,T., Hori,F., Iida,J., Imamura,K., Imotani,K., Ishii,Y.,
 Itoh,M., Kagawa,I., Kanagawa,S., Katoh,H., Kawai,T.,
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 Nakamura,M., Nishi,K., Nomura,K., Numaaki,R., Ohno,M., Osaoto,N.,
 Ota,Y., Saitoh,H., Sakai,C., Sakai,C., Sakazume,N., Sano,H.,
 Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T.,

Tue Jul 25 10:09:05 2006

us-10-713-648a-29.rst

Sogabe, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F.,
Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K.,
Yasunishi, A. and Hayashizaki, Y.

FEATURES

SOURCE

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/organism="Oryza sativa (japonica cultivar-group)"
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callus (Normalized Library)"

ORIGIN

Query Match 16.4%; Score 604; DB 5; Length 650;
Best Local Similarity 97.4%; Pred. No. 3.3e-108;
Matches 637; Conservative 0; Mismatches 10; Indels 7; Gaps 2;

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1 GCGCGTCGACGACACCTCGGCGCTTTCACACACCGCGCTCGCGCGCTTCGCGCG 60
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61 CCTCTCAACGGCCCTTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120
3104 CTCCCGGCGCGCGCTTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3163
121 CTCCCGGCGCGCGCTTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
3164 CGGCGCTTTCGCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3223
181 TGCGCGCTTTCGCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 240
3224 CCTCTCTGCGCGCGCTTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3283
241 CCTCTCTGCGCGCGCTTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300
3284 CGGCGGAGAGCGCTTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3343
301 CGGCGGAGAGCGCTTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360
3344 CTCCGACGCGCGCGCTTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3403
361 CTCCGACGCGCGCGCTTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 416
3404 CACCTGATGAAACCTCAAGAAATTCATACACAGAAATTAATTAATTAATTAAT 3463
417 CACCTGATGAAACCTCAAGAAATTCATACACAGAAATTAATTAATTAATTAAT 476
3464 TACTGCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3523
477 TACTGCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 536
3524 GAG--TTAGGCAATTCAGATTTCAGAGAGTCCGCTTCTGTAATTTTGTAGT 3580
537 GAGTTTATGATTCAGATTTCAGAGAGTCCGCTTCTGTAATTTTGTAGT 596
3581 TTGTAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3634
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RESULT 5
LOCUS C1146832 599 bp mRNA linear EST 05-FEB-2006
DEFINITION C1146832 Oryza sativa (japonica cultivar-group) mixed shoot
(Normalized Library) Oryza sativa (japonica cultivar-group) cDNA
clone 028-M090R-B07 3', mRNA sequence.
ACCESSION C1146832
VERSION C1146832.1 GI:86504199
KEYWORDS EST.

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BPF
clade; Ehrhartoideae; Oryzae; Oryza.

REFERENCE

1 (bases 1 to 599)

AUTHORS

Kikuchi, S.

TITLE

Collection and mapping of over 30,000 transcription units by the
rice full-length cDNA project from japonica rice

JOURNAL

Unpublished (2006)

COMMENT

Contact: Shoshi Kikuchi
Department of Molecular Genetics, Head of Laboratory of Gene
Expression
National Institute of Agrobiological Sciences
2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan
Tel: 81-29-838-7007
Fax: 81-29-838-7007
Email: skikuchi@ias.affrc.go.jp
This EST clone is one of 780k ESTs of Rice full length cDNA project
URL: <http://cdna01.dna.affrc.go.jp/cdna/>
NIAS Rice Full-length cDNA Project Team: Kikuchi, S., Satoh, K.,
Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J.,
Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T.,
Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T.,
Yamamoto, M. and Nakahama, Y.

FAIS Genome Sequencing & Analysis Group: Oromo, Y., Iida, Y.,
Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M.,
Kodama, T., Kuroseki, T., Kusumegi, T., Lu, M., Masuda, H., Miura, J.,
Mizuno, K., Nariikawa, R., Nikiura, Y., Oka, M., Ryu, R., Sugano, S.,
Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S.,
Yoshimura, A., Matsubara, K. and Murakami, K.
Genome Exploration Research Group in Riken Genomic Sciences Center
and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K.,
Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T.,
Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K.,
Hirooka, T., Hori, F., Iida, J., Imanishi, K., Imotani, K., Ishii, Y.,
Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J.,
Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Konda, M.,
Koya, S., Kurimura, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Nunasaki, N., Ohno, M., Otsu, N.,
Ota, Y., Satoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H.,
Sasaki, D., Sato, K., Shibata, K., Shingawa, A., Shiraki, T.,
Sogabe, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F.,
Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K.,
Yasunishi, A. and Hayashizaki, Y.

FEATURES

SOURCE

1. 599
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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shoot (Normalized Library)"

ORIGIN

Query Match 15.2%; Score 557.8; DB 5; Length 599;
Best Local Similarity 97.7%; Pred. No. 4.2e-99;
Matches 589; Conservative 0; Mismatches 7; Indels 7; Gaps 2;

2996 CACCTCGGCGCTTTCACACCGCGCTCGCGCGCGCTTCGCGCGCGCTTCACCGG 3055
1 CACCTCGGCGCTTTCACACCGCGCTCGCGCGCGCTTCGCGCGCGCTTCACCGG 60
3056 CCTCTTCGCGAGCCACCTCTGCAACCTCTTCTCCCGTGCAGACTCCCGGCGCGC 3115
61 CCTCTTCGCGAGCCACCTCTGCAACCTCTTCTCCCGTGCAGACTCCCGGCGCGC 120
3116 CTCTTACG 3175
121 CTCTTACG 180

RESULT 7	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
Oy	3176	CGTGGCCCTGGAAACGCGTCGTGACCTCCCTCATCTGCTCGGCACATCAACCTTCCTGTC	C1145244	650 bp	mRNA	linear	EST 05-FEB-2006					
Db	181	CGTGGCCCTGGAAACGCGTCGTGACCTCCCTCATCTGCTCGGCACATCAACCTTCCTGTC	C1145244	650 bp	mRNA	linear	EST 05-FEB-2006					
Oy	3236	GCTCCGACATGCCCCGACGACAGCTCGAGCTCGGCGACGACGCGCTCCGACGAGAGC	C1145244	650 bp	mRNA	linear	EST 05-FEB-2006					
Db	241	GCTCCGACATGCCCCGACGACAGCTCGAGCTCGGCGACGACGCGCTCCGACGAGAGC	C1145244	650 bp	mRNA	linear	EST 05-FEB-2006					
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Db	537	ATTGCACTTTGCAAGTTTACGTCGTATTTAACACGCGCGCTGGAGTTTAACT	C1145244	650 bp	mRNA	linear	EST 05-FEB-2006					
Oy	3593	ATA 3595	C1145244	650 bp	mRNA	linear	EST 05-FEB-2006					
Db	597	ATA 599	C1145244	650 bp	mRNA	linear	EST 05-FEB-2006					

Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K., Akimura, T., Arikawa, T., Carninci, P., Fukuda, S., Hanagaki, T., Hara, A., Haseizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Iida, J., Imamura, K., Imotani, K., Ishii, Y., Itoh, M., Kawana, I., Kanagawa, S., Katoh, H., Kawai, J., Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ono, M., Osato, N., Ota, Y., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibata, K., Shimagawa, A., Shiraki, T., Sobabe, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K., Yasunishi, A. and Hayashizaki, Y.									
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	/tissue="028-M06R-E06"								
	/clone_lib="mixed shoot (Normalized library)"								
	/clone_lib="Oryza sativa (japonica cultivar-group) mixed shoot (Normalized library)"								
ORIGIN									
Query Match	15.1%	Score 556.4;	DB 5;	Length 650;					
Best Local Similarity	98.3%	Pred. No. 8.1e-99;							
Matches 574;	Conservative 0;	Mismatches 6;	Indels 4;	Gaps 1;					
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Db	124	GTGGTACACCATGATGATTCCTCCACAAGCGCTCCAGATCTTGACGGCGGTGACGAC	183						
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Db	304	CTACGGCGGCGCGCGGCGCGCGAGTTCCGACAGACAGATCGCGGCGCTTCTGTGT	363						
OY	3179	CGCCTGGAAGCTGTCGTTCACCTCCCTCATGTGCTTGCCTTCCCATCAACTCTCTGTCGGCT	3238						
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OY	3239	CCGATGCGCGACGACAAGCTCGAGGTTCGGGACGAGCGCGTTCACGGCGGAGGGCCTA	3298						
Db	424	CCGATGCGCGACGACAAGCTCGAGGTTCGGGACGAGCGCGTTCACGGCGGAGGGCCTA	483						
OY	3299	CGCGCTCTGGGGGCGACGGCGAGATGTACAGAGTCAACAAGCAGCGCTCCGACGCGCGCT	3358						
Db	484	CGCGCTCTGGGGGCGACGGCGGAGATGTACAGAGTCAACAAGCAGCGCTCCGACGCGCGCT	543						
OY	3359	TGCCCCGCTGTCGTATGATGATCACTTAATTCATATGTCATGTGCTGTCACTGATATAAAC	3418						
Db	544	TGCCCCGCTGTCGTATGATGATGATGAC-----ATTGACATGTGCTGTCACTGATATAAAC	599						
OY	3419	TCAGAAATTCATACACACAGAATTAATTAATCTAGCTTTGCTT	3462						
Db	600	TCAGAAATTCATACACACAGAATTAATTAATCTAGCTTTGCTT	643						

RESULT 8

CT275500

LOCUS C1275500 600 bp mRNA linear EST 08-FEB-2006
 DEFINITION C1275500 Oryza sativa (japonica cultivar-group) mixed callus
 (Normalized Library) Oryza sativa (japonica cultivar-group) cDNA
 clone 077-M143R-D09 3', mRNA sequence.
 ACCESSION C1275500
 VERSION C1275500.1 GI:87015310
 KEYWORDS EST.
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BPP
 clade; Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 600)
 Kikuchi, S.
 Collection and mapping of over 30,000 transcription units by the
 rice full-length cDNA project from japonica rice
 Unpublished (2006)
 CONTACT Shoshi Kikuchi
 DEPARTMENT Department of Molecular Genetics, Head of Laboratory of Gene
 Expression
 NATIONAL INSTITUTE OF AGROBIOLOGICAL SCIENCES
 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan
 TEL: 81-29-838-7007
 FAX: 81-29-838-7007
 EMAIL: skikuchi@ias.affrc.go.jp
 This EST clone is one of 780K ESTs of Rice full length cDNA Project
 URL: http://cdna01.dna.affrc.go.jp/cDNA/
 NIAS Rice Full-length cDNA Project Team: Kikuchi, S., Satoh, K.,
 Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yasaki, J.,
 Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T.,
 Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T.,
 Yamamoto, M., and Nakahama, Y.
 PAIS Genome Sequencing & Analysis Group: Otonari, Y., Iida, Y.,
 Fujimura, T., Ikeda, R., Ishibiki, Y., Kawamata, M., Kobayashi, M.,
 Kodama, T., Kurosaki, T., Kusumegi, T., Lu, M., Masuda, H., Miura, J.,
 Mizuno, K., Narikawa, R., Nishikura, J., Oka, M., Ryu, R., Sugano, S.,
 Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S.,
 Yoshimura, A., Matsubara, K., and Murakami, K.
 Genome Exploration Research Group in Riken Genomic Sciences Center
 and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K.,
 Akimura, T., Arikawa, T., Carninci, P., Fukuda, S., Hanagaki, T.,
 Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K.,
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 Sogabe, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F.,
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 Yasunishi, A., and Hayashizaki, Y.
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 Best Local Similarity 97.2%; Pred. No. 2.4e-98;
 Matches 587; Conservative 0; Mismatches 10; Indels 7; Gaps 2;
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 DB 1 CCCTCTGCAACCTCTTCTCCCTCCGCGAATCCCGGCGCGCTTCTTACGGCGCGCGCG 60
 QY 3133 GCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTTCTTCTGCTGCGCTCGAAGCGTGC 3192

DB 61 GCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTTCTTCTGCTGCGCTCGAAGCGTGC 120
 QY 3193 TCGTCACCTCCCTCATCTGCTCTCGCGATCACTCTCTCCGCTCCGATGCCGACG 3252
 DB 121 CCGTCACCTCCCTCATCTGCTCTCGCGATCACTCTCTCCGCTCCGATGCCGACG 180
 QY 3253 ACAAGCTCGAGCTCG 3312
 DB 181 ACAAGCTCGAGCTCG 240
 QY 3313 ACGCGAGATGTAACGATGTAACGATGTAACGATGTAACGATGTAACGATGTAACGATG 3372
 DB 241 ACGCGAGATGTAACGATGTAACGATGTAACGATGTAACGATGTAACGATGTAACGATG 300
 QY 3373 TATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3432
 DB 301 TATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 356
 QY 3433 CACACGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3492
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 QY 3493 AGTTTACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3549
 DB 417 AGTTTACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 476
 QY 3550 CAGGGAGTCCCGGCTCTGATTTTGTGATTTTGTGATTTTGTGATTTTGTGATTTTGTGAT 3609
 DB 477 CAGGGAGTCCCGGCTCTGATTTTGTGATTTTGTGATTTTGTGATTTTGTGATTTTGTGAT 536
 QY 3610 CTTACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3669
 DB 537 CTTACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 596
 QY 3670 TTCC 3673
 DB 597 TTCC 600

RESULT 9
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 DEFINITION C1277861 Oryza sativa (japonica cultivar-group) mixed shoot
 (Normalized Library) Oryza sativa (japonica cultivar-group) cDNA
 clone 078-M145R-F04 3', mRNA sequence.
 ACCESSION C1277861
 VERSION C1277861.1 GI:87020129
 KEYWORDS EST.
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BPP
 clade; Ehrhartoideae; Oryzaceae; Oryza.
 1 (bases 1 to 639)
 Kikuchi, S.
 Collection and mapping of over 30,000 transcription units by the
 rice full-length cDNA project from japonica rice
 Unpublished (2006)
 CONTACT Shoshi Kikuchi
 DEPARTMENT Department of Molecular Genetics, Head of Laboratory of Gene
 Expression
 NATIONAL INSTITUTE OF AGROBIOLOGICAL SCIENCES
 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan
 TEL: 81-29-838-7007
 FAX: 81-29-838-7007
 EMAIL: skikuchi@ias.affrc.go.jp
 This EST clone is one of 780K ESTs of Rice full length cDNA Project
 URL: http://cdna01.dna.affrc.go.jp/cDNA/
 NIAS Rice Full-length cDNA Project Team: Kikuchi, S., Satoh, K.,
 Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yasaki, J.,
 Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T.,
 Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T.,

Yamamoto, M. and Nakahama, Y.
FAIS Genome Sequencing & Analysis Group: Ootomo, Y., Iida, Y.,
Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M.,
Kodama, T., Kurosaki, T., Kusumegi, T., Lu, M., Masuda, H., Mura, J.,
Mizuno, K., Narikawa, R., Nishikawa, J., Oka, M., Ryu, R., Sugano, S.,
Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S.,
Yoshimura, A., Matsubara, K. and Murakami, K.
Genome Exploration Research Group in Riken Genomic Sciences Center
and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K.,
Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T.,
Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K.,
Hirooka, T., Hori, F., Iida, J., Imamura, K., Imotani, K., Ishii, Y.,
Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J.,
Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
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Ota, Y., Satoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H.,
Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T.,
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Takahara, A., Tanaka, T., Tomaru, A., Toya, T., Waki, K.,
Yaenishi, A. and Hayashizaki, Y.
Location/Qualifiers
1. 639
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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/clone="078-M145R-F04"
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/clone_lib="Oryza sativa (japonica cultivar-group) mixed
shoot (Normalized library)"

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Query Match 15.0%; Score 551.8; DB 5; Length 639;
Best Local Similarity 98.0%; Pred. No. 6.5e-98;
Matches 581; Conservative 0; Mismatches 7; Indels 5; Gaps 2;
2879 TGCAGGGGGTGTGCAGGGGGTGGGGGGTGGTGTGATGGGGGGTGGCGGGAGCATGCC 2938
51 TGCAGGGGGTGTGCAGGGGGTGGGGGGTGGTGTGATGGGGGGTGGCGGGAGCATGCC 110
2939 GTGTATACACATGATGATCTCTCCACAAAGCGCTTCCAGATCTTGCAGCGGTGCAGCAC 2998
111 GTGTATACACATGATGATCTCTCCACAAAGCGCTTCCAGATCTTGCAGCGGTGCAGCAC 170
2999 CCTGGCGCTTCTTCCACACCCACCGCGCTGGCGCTCTTGGGGGCTTCTTCAACGGGCTT 3058
171 CCTGGCGCTTCTTCCACACCCACCGCGCTGGCGCTCTTGGGGGCTTCTTCAACGGGCTT 230
3059 CTTGGCGGACCCACCTCTGCAACTCTTCCCTCCCGCGCGGCACTCCCGGGGGGCTT 3118
231 CTTGGCGGACCCACCTCTGCAACTCTTCTCTCCCGCGCGGCACTCCCGGGGGGCTT 290
3119 CTACGGCGGCGCGCGCGCGCGCGCGAGTTGCGCAAGCATGCGCGCGGCTTCTTGTGCT 3178
291 CTACGGCGGCGCGCGCGCGCGCGCGAGTTGCGCAAGCATGCGCGCGGCTTCTTGTGCT 350
3179 CGCCTTGGAAGCTGTGTGATCTCTCTCTGCTGTGCTGCGCATCACTTCTGCTCCGCT 3238
351 CGCCTTGGAAGCTGTGTGATCTCTCTCTGCTGTGCTGCGCATCACTTCTGCTCCGCT 410
3239 CGCGATGCCCGAGCAAGCTGAGAGTGGGCGAGCGAGCGGCTCAACGGGAGGAGGCTTA 3298
411 CGCGATGCCCGAGCAAGCTGAGAGTGGGCGAGCGAGCGGCTCAACGGGAGGAGGCTTA 470
3299 CGCGCTCTGGGGGCGAGCGGAGAGTGTATCGACGTCACCAAGCAGGCTCCGACGCGCGCT 3358
471 CGCGCTCTGGGGGCGAGCGGAGAGTGTATCGACGTCACCAAGCAGGCTCCGACGCGCGCT 530
3359 TGGCCCGCTGTGTGTATGATCGATCATTATGTCATGTGCTGTCACTGTATGAATCC 3418
531 TGGCCCGCTGTGTGTATGATCGATCATTATGTCATGTGCTGTCACTGTATGAATCC 586

QY 3419 T-CAGGAATTCATACACAGAAATTAATACTAGCTTTGCTTCACTGCT 3470
DB 587 TCCAGAAATTCATACACAGAAATTAATACTAGCTTTGCTTCACTGCT 639
RESULT 10
C1142521
LOCUS
DEFINITION
C1142521 Oryza sativa (japonica cultivar-group) mixed shoot
(Normalized library) Oryza sativa (japonica cultivar-group) cDNA
clone 028-M029R-D05 3', mRNA sequence.
C1142521
C1142521.1 GI:86499888
EST
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP
clade; Ehrhartoidae; Oryzaceae; Oryza.
1 (bases 1 to 581)
Kikuchi, S.
Collection and mapping of over 30,000 transcription units by the
rice full-length cDNA project from japonica rice
Unpublished (2006)
Contact: Shoshi Kikuchi
Department of Molecular Genetics, Head of Laboratory of Gene
Expression
National Institute of Agricultural Sciences
2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan
Tel: 81-29-838-7007
Fax: 81-29-838-7007
Email: skikuchi@nias.affrc.go.jp
This EST clone is one of 780k ESTs of Rice full length cDNA Project
URL: <http://cdna01.dna.affrc.go.jp/cDNA/NIAS>
Rice Full-length cDNA Project Team: Kikuchi, S., Satoh, K.,
Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J.,
Ishikawa, M., Yamada, H., Ooka, H., Horita, I., Kojima, K., Shimiki, T.,
Ohneda, E., Yabagi, W., Suzuki, K., Li, C., Ohsuiki, K., Shishiki, T.,
Yamamoto, M. and Nakahama, Y.
FAIS Genome Sequencing & Analysis Group: Ootomo, Y., Iida, Y.,
Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M.,
Kodama, T., Kurosaki, T., Kusumegi, T., Lu, M., Masuda, H., Mura, J.,
Mizuno, K., Narikawa, R., Nishikawa, J., Oka, M., Ryu, R., Sugano, S.,
Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S.,
Yoshimura, A., Matsubara, K. and Murakami, K.
Genome Exploration Research Group in Riken Genomic Sciences Center
and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K.,
Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T.,
Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K.,
Hirooka, T., Hori, F., Iida, J., Imamura, K., Imotani, K., Ishii, Y.,
Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J.,
Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Otsu, N.,
Ota, Y., Satoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H.,
Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F.,
Takahara, A., Tanaka, T., Tomaru, A., Toya, T., Waki, K.,
Yaenishi, A. and Hayashizaki, Y.
Location/Qualifiers
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/cultivar="Nipponbare"
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shoot (Normalized library)"

ORIGIN
Query Match 14.6%; Score 535.6; DB 5; Length 581;
Best Local Similarity 98.0%; Pred. No. 1e-94;

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Matches 575; Conservative 0; Mismatches 5; Indels 7; Gaps 3;
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DB 1 GATGGGGGTGCTCGCCGCGAGCATCCGCTGGTACACATGATGATCTTCCACAAGGCTTC 60
QY 2972 CAAGATTCCTGACAGCGGTGCGAGCAACCGTGGCGCTTCCACACCCACAGGGGTGCGCG 3031
DB 61 CAAGATTCCTGACAGCGGTGCGAGCAACCGTGGCGCTTCCACACCCACAGGGGTGCGCG 120
QY 3032 CCTCTCTCGAGCGGCTCTCTACCGGCTCTTCCGCGAGCCACCTCTGCAACCTCTTCTCT 3091
DB 121 CCTCTCTCGAGCGGCTCTCTACCGGCTCTTCCGCGAGCCACCTCTGCAACCTCTTCTCT 180
QY 3092 CCCCCTGCGCACTCCCGGGGCGCTTCTTACGCGGCGCGCGCGCGCCCACTTCCGCA 3151
DB 181 CCCCCTGCGCACTCCCGGGGCGCTTCTTACGCGGCGCGCGCGCGCCCACTTCCGCA 240
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DB 241 GAGATGCGCCCGGCGCTCTCTCTGCTGCTGCGCTGGAACCTGCTCTCACTCCCTCATCT 300
QY 3211 GCTCTGCGCATCAACCTCTCTCTGCTGCTGCGCTGGAACCTGCTCTCACTCCCTCATCT 3270
DB 301 GCTCTGCGCATCAACCTCTCTCTGCTGCTGCGCTGGAACCTGCTCTCACTCCCTCATCT 360
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QY 3331 TCACCAAGACGCGCTTCCAGCGCGCGCTGCGCTGCTGATGATGATGATGATGATGAT 3390
DB 421 TCACCAAGACGCGCTTCCAGCGCGCGCTGCGCTGCTGATGATGATGATGATGATGAT 476
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DB 477 TTGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 536
QY 3451 ACGTGTTCCTTCTACTGCTTAATTATGAAATCTATGTTCAAGTTT 3497
DB 537 ACGTGTTCCTTCTACTGCTTAATTATG--AATCTATGTTCAAGTTT 581

RESULT 11
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DEFINITION OSUNBE16H13.f OSUNBE Oryza sativa (japonica cultivar-group) cDNA
VERSION CB678450.1 GI:29682175
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Bep
1 (bases 1 to 589)
Jantanasubivat,C., Gowda,M., Haller,K., Hatfield,J., Lu,G.,
Stalberg,E., Zhou,B., Li,H., Kim,H., Yu,Y., Dean,R.A., Wang,R.A.,
Soderlund,C., and Wang,G.L.
Large-scale identification of expressed sequence tags involved in
rice and rice blast fungus interaction
Plant Physiol. 138 (1), 105-115 (2005)
1588683
TITLE Contact: Rod Wing
JOURNAL Arizona Genomics Institute
PUBMED University of Arizona
COMMENT Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: rwing@genome.arizona.edu
PCR Primers
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FORWARD: gta aaa cga cgg cca gtc
BACKWARD: gga aac agc tat gac cat g
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Location/Qualifiers
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XhoI, 24 hrs after inoculation with Rice Blast (70-15)"

ORIGIN
Query Match 14.5%; Score 531.4; DB 4; Length 589;
Best Local Similarity 96.1%; Pred. No. 6.8e-94;
Matches 568; Conservative 0; Mismatches 16; Indels 7; Gaps 2;

QY 3066 GAGCCCAACCTCTGCAACCTCTTCCCTCCCGCGCGCACTCCGCGGCGCCTTCTTACGCG 3125
DB 589 GAGCCCAACCTCTGCAACCTCTTCCCTCCCGCGCGCACTCCGCGGCGCCTTCTTACGCG 530
QY 3126 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3185
DB 529 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 470
QY 3186 AACGTGCTGCTCACTCTCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3245
DB 469 AACGTGCTGCTCACTCTCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 410
QY 3246 CCCGACGCAACCTGAGGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3305
DB 409 CCCGACGCAACCTGAGGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 350
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QY 3543 GCAATTCAGGGAGTCCGCTTCTGATTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 3602
DB 113 GCAATTCAGGGAGTCCGCTTCTGATTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 54
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RESULT 12
LOCUS C1179219 550 bp mRNA linear EST 06-FEB-2006
DEFINITION C1179219 Oryza sativa (japonica cultivar-group) supermix Oryza
sativa (japonica cultivar-group) cDNA clone 034-M062R-F07 3', mRNA
sequence.
ACCESSION C1179219
VERSION C1179219.1 GI:86539013
KEYWORDS EST.
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SOURCE
ORGANISM Oryza sativa (japonica cultivar-group)
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 Eurycotylae; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Bp
 clade; Eriophytidae; Oryzaceae; Oryza.
REFERENCE
AUTHORS Kikuchi, S.
TITLE Collection and mapping of over 30,000 transcription units by the
 rice full-length cDNA project from japonica rice
JOURNAL Unpublished (2006)
COMMENT Contact: Shoshi Kikuchi
 Department of Molecular Genetics, Head of Laboratory of Gene
 Expression
 National Institute of Agricultural Sciences
 2-1-2 Kamondai, Tsukuba, Ibaraki 305-8602, Japan
 Tel: 81-29-838-7007
 Fax: 81-29-838-7007
 Email: kikuchi@iaes.affrc.go.jp
 This EST clone is one of 780k ESTs of Rice full length cDNA project
 URL: http://cdna01.dna.affrc.go.jp/cdna/

FEATURES
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 supermix"
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 1 ATGATCTCCACAGGCTCTCAAGATCTGCAAGCGGTGACGACACCTCGCGCTTC 60
 3012 CACACCCACAGGCTGCGCGCTCTGCGCGCTCTGACCGCTCTTTCGCGAGCC 3071
 61 CACACCCACAGGCTGCGCGCTCTGCGCGCTCTGACCGCTCTTTCGCGAGCC 120
 3072 ACCCTCTGCAACCTCTTCTCCCGTCCGCGACTCCCGGGGCGCTTTCGCGAGCC 3131
 121 ACCCTCTGCAACCTCTTCTCCCGTCCGCGACTCCCGGGGCGCTTTCGCGAGCC 180

ORIGIN
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 Best Local Similarity 86.8%; Pred. No. 1.8e-92;
 Matches 577; Conservative 0; Mismatches 88; Indels 0; Gaps 0;
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FEATURES
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 Best Local Similarity 86.8%; Pred. No. 1.8e-92;
 Matches 577; Conservative 0; Mismatches 88; Indels 0; Gaps 0;
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 Best Local Similarity 86.8%; Pred. No. 1.8e-92;
 Matches 577; Conservative 0; Mismatches 88; Indels 0; Gaps 0;
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[illegible]

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QY	299	AGATGTCTCTCTCGGCGACCGGTGTGCCGTACGAGGGAACAGTCGCGGTGCG	358		
DB	127	TGTGTCGTCTCTCCGGGACGAGAGTCGCGCTGAGCTTACAG- - - -ACGTGGCGTGT	180		
QY	359	TGGCGGACTGCTGTAACAAGGGGACACACGCTGTGCACTGATGCGGCGACTGTGTG	418		
DB	181	CTCCGAGTGTCTGAACAAGGGGACACACGCTGTGCACTGAGCGGCGACGCTGTGTG	240		
QY	419	GCGTCGACAGCGTGTCCGGGCTTTGTGTGTCTGTATCGCGCGCTGTGTAAAGAAAGTGGG	478		
DB	241	GCGTCGACAGCTTCCGGGCTGTGTGTCTGTATCGCGCGCTGTGTAAAGAAAGTGGG	300		
QY	479	CGGTGAATTCGGGCTTTCAATGGCGCTTACAGCGCGCTTGCAGCGGTGTGATCTGTGGGTCA	538		
DB	301	CGGTGAATTCGCGCTTCAATGGCGCTGTACGCGGTTCGCGCGGTGTGATCTGTGGGTCA	360		
QY	539	CCTGGGCGTACAAACATGTCTGTTCGGGGAGAAAGCTTCCGATCTGCGGGAAAGCGCGGC	598		
DB	361	CCTGGGCGTACAAACATGTCTTTCGGCGACAGGCTGTGCGGTGTGTGGGCAAGCGCGGC	420		
QY	599	CGGCGCTGTGAACCAAGGGCTCTCTCGTTCGGCGCGCGCGCTGTGCGGCGACAGTCACTAC	658		
DB	421	CGGCGCTGTGAACCAAGGGCTGTGTGTGGGCAAGCGCGGCTTCCCGCCACAGGGGCAACCT	480		
QY	659	GCGCGGACGGGAGCGGTGAGACGCGCGCGGTGTGAGACCGCTGTACCGGATGTGCGAGCTGTG	718		
DB	481	TGCGCAGCGGCGCTGTGAGAACCCGCGCGCGGAGCCGCTGTATCCGATGTGCGACAGTGTG	540		
QY	719	TGTACTTCAGTGTGTGTGTGCGCGGCATCACCTTCATCTGTGTGCGCGGCTTCTTCTCTG	778		
DB	541	TGTACTTCAGTGTGTGTGTGCGCGGCATCACCTGTGTCTGTGTGTGCGCGGCTTCTTCTCTG	600		
QY	779	GCGCGATAGAGCTTCTCGCGCTGTGATGATCTTGTCCCGCTCTGTGCTACCTTCTCTTCA	838		
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DB	661	CGGTGTGCGGCTTCTCTCGTATGTGGGCGCGGCTTCTTTCAGTGTGGGCGGTCAATCACT	720		
QY	899	ACTGTGCGCGGCTAGCTATCAAGTCTTCCGCGCGGATGTGCGGCTTCAACGCGCGCTTACT	958		
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ACCESSION DX307908 GI:85584678
VERSION DX307908.1 GI:85584678
KEYWORDS GSS.
SOURCE Oryza ridleyi
ORGANISM Oryza ridleyi
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BPP
clade; Ehrhartoideae; Oryzaceae; Oryza.
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Kim,H., Collura,K., Wisotski,M., Byrne,M., Stum,D., Smart,D.,
Rao,K., Luo,M., Jetty,R., Kudrna,D., Muller,C., Soderlund,C. and
Wing,R.
OMP (Oryza Map Alignment Project) - Arizona Genomics Institute
Unpublished (2005)
TITLE Oryza Map Alignment Project - Arizona Genomics Institute
JOURNAL
COMMENT
Contact: Rod A. Wing
Arizona Genomics Institute
University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9595
Fax: 520 621 1259
Email: rwing@genome.arizona.edu
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Query Match 13.5%; Score 497.8; DB 14; Length 685;
Best Local Similarity 91.5%; Pred. No. 2,9e-87;
Matches 561; Conservative 0; Mismatches 47; Indels 5; Gaps 3;

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OY 366 CTGGCTGAACAAGGGGGAACAACCGTGGCACTGTGGGGGCGGACCGCTGGGGCTGCA 425
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OY 426 GAGCGTGGCGGCTTGT 485
DB 182 GAGCGTGGCGGCTTGT 241
OY 486 CTCGGGCTTCATGTGGCGCTCTACGCCCTTTCGCGCGCGTGTGATCTGCTGGGTCACTGGGC 545
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DB 302 GTACAAACATGT 361
OY 606 GGACCGAGGCGCTCTGTGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 665
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OY 666 CGGCAAGCTGTGAACGCGCGCGGTGGAGCGCTGTACCCGATGGCGACGCGGTGTACTT 725
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OY 726 CCAAGTGGCTGTGGCGCGCATCACCGTCATCTGTGGCGCGGCTCCCTCGGCGCGCAT 785
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OY 786 GAGCTTCTCTGCTGATGATCTTGTCCGCTGTGCTACCTTCTCTACACCGTC-G 844
DB 542 GAGCTTCTCTGCTGATGATCTTGTCCGCTGTGCTACCTTCTCTACACCGTCG 601
OY 845 GCGCTTCTCTCTCTGGGG--CGGCGGCTTCTCTTCCACTGGGG--CGTATGACTAC 900
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DB 662 TGGCGGCGCTACG 674

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Job time : 16358 secs

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	289.6	7.9	1961	3	US-10-033-109-11
4	190.2	5.2	376	3	US-10-033-109-7
5	115.6	3.1	300	3	US-09-197-649-7
6	112.8	3.1	1368	3	US-09-252-991A-7174
7	111.8	3.0	1575	3	US-09-252-991A-7330
8	103	2.8	1926	3	US-09-249-585A-4
9	103	2.8	1931	2	US-09-130-114-2
10	97.2	2.6	380	3	US-09-197-649-7
11	91.6	2.5	987	3	US-09-252-991A-7285
12	90	2.4	4403765	3	US-09-103-840A-2
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14	89.8	2.4	1140	3	US-09-023-173-4
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16	88	2.4	546	3	US-09-252-991A-7284
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29	81.4	2.2	4547	3	US-09-410-551B-22	Sequence 22, Appl
30	81.4	2.2	4547	3	US-09-940-316B-22	Sequence 22, Appl
31	81.4	2.2	4571	3	US-09-410-551B-18	Sequence 18, Appl
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35	80.8	2.2	3489	2	US-08-728-327A-1	Sequence 1, Appl
36	80.8	2.2	3489	3	US-09-298-568-1	Sequence 1, Appl
37	80.8	2.2	3489	3	US-09-410-399-1	Sequence 1, Appl
38	80.8	2.2	3489	3	US-09-894-272-1	Sequence 1, Appl
39	80.8	2.2	32207	2	US-08-770-379-20	Sequence 20, Appl
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41	80.8	2.2	32207	3	US-09-230-371A-20	Sequence 20, Appl
42	80.6	2.2	1138	3	US-08-581-148C-3	Sequence 3, Appl
43	78.6	2.1	77536	3	US-09-410-551B-1	Sequence 1, Appl
44	78.6	2.1	77536	3	US-09-940-316B-1	Sequence 1, Appl
45	78.4	2.1	1189	3	US-10-379-010-7	Sequence 7, Appl

ALIGNMENTS

RESULT 1
US-10-033-109-13
Sequence 13, Application US/10033109
Patent No. 6833492
GENERAL INFORMATION:
APPLICANT: Allen, Stephen M.
APPLICANT: Rafalski, J. Antoni
APPLICANT: Sakai, Hajime
TITLE OF INVENTION: Nitrogen Transport Metabolism
FILE REFERENCE: BB-1210
CURRENT APPLICATION NUMBER: US/10/033,109
CURRENT FILING DATE: 2001-12-28
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/384,625
PRIOR FILING DATE: EARLIER FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/098,248
PRIOR FILING DATE: EARLIER FILING DATE: 28 August 1998
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Microsoft Office 97
SEQ ID NO 13
LENGTH: 1656
TYPE: DNA
ORGANISM: Trifolium aestivum
US-10-033-109-13

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Best Local Similarity 86.9%; Pred. No. 8.8e-99;
Matches 582; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

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DB	143	CTGGGCTGAACAGGGGGAACAGCGCGGAGCTGGGCGCGGACGCTGGGCGTGA	202
QY	426	GAGCGTCCGCGGCTTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG	485
DB	203	GAGCGTCCGCGGCGATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG	262
QY	486	CTGCGGCTTCAGGCGCTTCAGGCGCTTCAGGCGCTTCAGGCGCTTCAGGCGCT	545
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QY	546	GTACCAATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC	605

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Qy 606 GAGCAGAGGCTTCCTGTCGCGCGCGCGCTGCGCGAGCTCACTACCGCGCGA 665
Db 383 CGACACAGGCTTCCTGTCGCGCGCGCGCTGCGCGAGCTCACTACCGCGCGA 442
Qy 666 CGGACGCTGAGAGAGGCGCGCGCGCTGAGAGCTCACTACCGAGAGGAGTACTT 725
Db 443 CGGACGCTGAGAGAGGCGCGCGCGCTGAGAGCTCACTACCGAGAGGAGTACTT 502
Qy 726 CAGTGCCTGTCGCGCGAGCTCACTGCTGCGCGCGCTGCTGCTGCGCGAGT 785
Db 503 CAGTGCCTGTCGCGCGAGCTCACTGCTGCGCGCGCTGCTGCTGCGCGAGT 562
Qy 786 GAGCTTCCTGCGCGAGTATCTTCTGCTGCGCGCTGCTGCTGCTGCTGCTGCTG 845
Db 563 GAGCTTCCTGCGCGAGTATCTTCTGCTGCGCGCTGCTGCTGCTGCTGCTGCTG 622
Qy 846 GCGCTTCCTGCGCGAGTATCTTCTGCTGCGCGCTGCTGCTGCTGCTGCTGCTG 905
Db 623 GCGCTTCCTGCGCGAGTATCTTCTGCTGCGCGCTGCTGCTGCTGCTGCTGCTG 682
Qy 906 CGGCTACGTCATCAAGTCTGCGCGCGAGTCCGCGCTTCACTGCGCTTACGCGTCCG 965
Db 683 CGGCTACGTCATCAAGTCTGCGCGCGAGTCCGCGCTTCACTGCGCTTACGCGTCCG 742
Qy 966 TACTACACAGC 975
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RESULT 2
US-10-033-109-9
; Sequence 9, Application US/10033109
; Patent No. 6833492
; GENERAL INFORMATION:
; APPLICANT: Allen, Stephen M.
; APPLICANT: Rafalski, J. Antoni
; APPLICANT: Sakai, Hajime
; TITLE OF INVENTION: Nitrogen Transport Metabolism
; FILE REFERENCE: BB-1210
; CURRENT APPLICATION NUMBER: US/10/033,109
; PRIORITY FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/384,625
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/098,248
; PRIOR FILING DATE: EARLIER FILING DATE: 28 August 1998
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 9
; LENGTH: 1883
; TYPE: DNA
; ORGANISM: Oryza sativa
US-10-033-109-9

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Best Local Similarity 74.0%; Pred. No. 5.5e-70;
Matches 493; Conservative 0; Mismatches 173; Indels 0; Gaps 0;

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Db 194 CGGCGCTGCAATGCTGCGCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 253
Qy 477 GGGGCTGCAATGCTGCGCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 536

Db 254 GCGCGTCACTCGGCTTATGCGCTGTGAGCGCTGACCGCTGACCGCTCATCTGTGGGT 313
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Qy 657 CCGCGCGAGAGAGGCTTCCGAGAGAGAGAGAGCTCCTCCGATCTGAGGAGAGGCG 716
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Qy 717 GGTGACTTCCAGTGTGCTTCCGAGAGAGAGAGCTCCTCCGATCTGAGGAGAGGCG 776
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Db 554 CCGAGAGATGAACATCAAGGCTGAGAGAGAGCTTCACTCCGCTGAGGAGAGGCG 613
Qy 837 CACGCTGCGCTTCTGCGCGAGAGAGAGAGCTTCTTCACTGAGGAGAGGCG 896
Db 614 CACGCTGCGCTTCTGCGCGAGAGAGAGAGAGCTTCTTCACTGAGGAGAGGCG 673
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; Sequence 11, Application US/10033109
; Patent No. 6833492
; GENERAL INFORMATION:
; APPLICANT: Allen, Stephen M.
; APPLICANT: Rafalski, J. Antoni
; APPLICANT: Sakai, Hajime
; TITLE OF INVENTION: Nitrogen Transport Metabolism
; FILE REFERENCE: BB-1210
; CURRENT APPLICATION NUMBER: US/10/033,109
; PRIORITY FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/384,625
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/098,248
; PRIOR FILING DATE: EARLIER FILING DATE: 28 August 1998
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 11
; LENGTH: 1961
; TYPE: DNA
; ORGANISM: Glycine max
US-10-033-109-11

Query Match 7.9%; Score 289.6; DB 3; Length 1961;
Best Local Similarity 67.0%; Pred. No. 1.6e-49;
Matches 409; Conservative 0; Mismatches 201; Indels 0; Gaps 0;

Qy 353 GGTGGCGAGTGTGAGCAAGAGGAGCAACGCGTGGAGCTGTGCGCGAGAGC 412
Db 248 CGGCGGACCCCAAGTGTGAGCAAGAGGAGCAACGCGTGGAGCTGTGCGCGAGAGC 307
Qy 413 TGTGGGCTGAGAGAGGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 472
Db 308 TGTGGGCTTGAAGAGATGCGGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 367
Qy 473 AGTGGCGGTGAGTGTGCGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 532

DB 368 AATGGGAGTGAATCACTGCTTTCAGCCCTTTGGGGGTTCTAATATGT 427
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DB 428 GGGTGTCTGGTGTATCCGAATGGCCTTGGAGAGAACTTTTCCCTTCTGGGGAAGG 487
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QY 773 TCTGTGGCGGCAATGACTTCTGCGCTGTATGATCTTCTGCGCGCTGTGTGTGTGT 832
DB 668 TCTTGTGGCGAATGAACATCAAGGCTTGTGTGTGTGTGTGTGTGTGTGTGTGT 727
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DB 728 CCTACACAGTGGGGCTTTTATGCTTTGGGGTGTGGCTTTCTTACCAATGGGGCGTTA 787
QY 893 TCGACTACTGCGGCGGCTACGTATCAAGTCTGCGCGGCAATGCGCGCTTACCGCGG 952
DB 788 TTGATATTCTGCGGCTATGTCATACACTTTCTTCTGGAATGCGTGGCTTCACTGCTG 847
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RESULT 4
US-10-033-109-7

Sequence 7, Application US/10033109

Patent No. 6833492

GENERAL INFORMATION:

APPLICANT: Allen, Stephen M.

APPLICANT: Rafalski, J. Antoni

APPLICANT: Sakai, Hajime

TITLE OF INVENTION: Nitrogen Transport Metabolism

FILE REFERENCE: BB-1210

CURRENT APPLICATION NUMBER: US/10/033,109

PRIOR FILING DATE: 2001-12-28

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/384,625

PRIOR FILING DATE: EARLIER FILING DATE: 1999-08-27

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/098,248

PRIOR FILING DATE: EARLIER FILING DATE: 28 August 1998

NUMBER OF SEQ ID NOS: 14

SOFTWARE: Microsoft Office 97

SEQ ID NO 7

LENGTH: 376

TYPE: DNA

ORGANISM: Zea mays

FEATURE:

NAME/KEY: unsure

LOCATION: (40)

NAME/KEY: unsure

LOCATION: (272)

NAME/KEY: unsure

LOCATION: (276)

NAME/KEY: unsure

LOCATION: (294)

NAME/KEY: unsure

LOCATION: (339)

NAME/KEY: unsure

LOCATION: (341)

NAME/KEY: unsure

LOCATION: (359)

NAME/KEY: unsure

LOCATION: (361)
US-10-033-109-7

Query Match 5.2%; Score 190.2; DB 3; Length 376;

Best Local Similarity 74.5%; Pred. No. 1,9e-29; Mismatches 85; Indels 10; Gaps 3;

Matches 277; Conservative 0;

QY 239 GCTAGTAGATATCAAAAAGGATTCAGAGCTTGTGTGTGTATCATCGAGCA 298
DB 1 GCTAAGAGAGAGAGAGAGATATCGTAGACCCAGCACTAGCTAATACCA 60
QY 299 AGATGT 358
DB 61 TGT 114
QY 359 TGGCGGATGCTGTAAACAAGGGGAGCAACGCTGTGAGTGTGTGTGTGTGTGT 418
DB 115 CTCCGAGTGTGTGTAAACAAGGGGAGCAACGCTGTGAGTGTGTGTGTGTGT 174
QY 419 GGCTGAGAGCGT 478
DB 175 GGCTGAGAGCTTCCGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 234
QY 479 CGGTGAATCGGCGTTCATAGCGCTCTACGCTTGTGCGCGC--GTGTGTGTGTGTGT 536
DB 235 CGGTGAATCGGCGCTTCAATGCGCTGTACGCTTGTGCGCGCGGTGTGTGTGTGT 294
QY 537 CACTTGGGGGTAAACAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 594
DB 295 GACTTGGGGGTAAACAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 354
QY 595 CGGCGGCGCTG 606
DB 355 CGGCGGCGCTG 366

RESULT 5
US-09-197-649-7/c

Sequence 7, Application US/09197649

Patent No. 6194550

GENERAL INFORMATION:

APPLICANT: Gold, Larry

APPLICANT: Tuerk, Craig

APPLICANT: Prihnow, David

TITLE OF INVENTION: Systematic Polypeptide Evolution by Reverse Translation

FILE REFERENCE: NEX02/C1-CON

CURRENT APPLICATION NUMBER: US/09/197,649

PRIOR FILING DATE: 1998-11-23

PRIOR APPLICATION NUMBER: 07/829,461

PRIOR FILING DATE: 1992-01-31

PRIOR APPLICATION NUMBER: 07/739,055

PRIOR FILING DATE: 1991-08-01

PRIOR APPLICATION NUMBER: 07/561,968

EARLIER FILING DATE: 1990-08-02

NUMBER OF SEQ ID NOS: 26

SOFTWARE: Patentln Ver. 2.0

SEQ ID NO 7

LENGTH: 390

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Sequence

OTHER INFORMATION: having a 120 repeat of ACG flanked by fixed

OTHER INFORMATION: fragments having NcoI restriction sites.

US-09-197-649-7

Query Match 3.1%; Score 115.6; DB 3; Length 390;

Best Local Similarity 57.5%; Pred. No. 4.1e-14;

Matches 208; Conservative 0; Mismatches 154; Indels 0; Gaps 0;

QY 3012 CACACCCAGCGGTGCGGGCTCTCGGCGGCTCTTACCGGCTTTCGCGGAGCC 3071

[illegible]

RESULT 6
 US-09-252-991A-7174
 ; Sequence 7174, Application US/09252991A
 ; Patent No.6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 10/7196,136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 7174
 ; LENGTH: 1368
 ; TYPE: DNA
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-7174

	Query Match	3.1%	Score 112.8	DB 3	Length 1368
	Best Local Similarity	51.2%	Pred. No. 2.9e-18		
	Matches 338	Conservative 0	Mismatches 292	Indels 30	Gaps 2
Qy	298	AAGATGTCGTCTCGGCGCAGGTGTGTCGCCGCTGCCTACAGGGGAAACAGTCGGCGTC	357		
Db	52	AAGATCGAGGGCTTGAAGACCTTATGTGTCCTTCGCTTTCGCGGCGTCGCCCTTCGCCCC	111		
Qy	358	GTGGCGGACTGGCTGAACAAAGGGGGACAACGCGTGGACAGCTGTGGCGCGACGCGTGG	417		
Db	112	GAGAGGCCCTTCCTTCAACAGCGGCGACACCGCTGGATGTATCTCCACTCCGCTCGTC	171		
Qy	418	GGGCTGCAGAGCGTCCCGGGCTTGTGTGTCCTGAACGGCGGCGTGTGAAGAAGAGTGG	477		
Db	172	CTGCTCATGACCATTCGCCGCGCTTCGCTTCTACGGCGGCGATGTGTGAACGAAGAAC	231		
Qy	478	GCGGTGAACCTCGGCGCTTACATGCGGCTCTACAGGCTTCGCGCGCGTGTGATCTGTGGGTC	537		
Db	232	GTGCTGTGATATATATGACAGTGCCTTCGCGCATACCGGCTGATATCACTTCTCTGGGTG	291		
Qy	538	ACCTGGGCGGTACAACATGTCCTTCGGGGAGAAAGCTCTCCGATCTGGGGGAAGGCGGG	597		
Db	292	GTTATATGCTAAGGCTCGCTGCTGATACCA-----CCGGG	327		

Qy	59	CGGCGCTGACAGAGGCTCTCTGTCGGCGCGCGGCTGCGGAGAGGCTCACTAC	657
Db	328	ATGAGAAAGGGCGTCTCTCAATTCAATTCTTTCTGGCGGAGCTGACAAAGGCTTCTC	387
Qy	658	CGGCGCGAGCGGAGCTGTAGACGGCGGGCGGTGAGACCTGTATCCCGATGGCGAGGTG	717
Db	388	AGGGGTCTAACCGCCGACGGCTGTACTTTCGCCACACGGCGCTGTCTCCGAAAGCGTTC	447
Qy	718	GTGTACTTCCAGTGGCGTGTTCGCCGCCCATCAACCTCATCTCTGTGCGGCGTCCCTCTC	777
Db	448	ATCACCTTCCAGATGACTTTCTCGCATATCACTCGGCGGTGATCGTCCGGCGCTTCGCC	507
Qy	778	GGCGGATAGCTTCTCGCGCTGATATATCTTCTGTCGCGCGCTGCGGCTCACCTTCTCTAC	837
Db	508	GAGCGATGAAGTTCTCGCGCATGCTGATCTTCAATGAGGATCTGTTTACACCGTGTAC	567
Qy	838	ACCGTGGGCGCTTCTCCCTCTGG-----GGCGGCGCTTCTCTTCACTGCGGCGTC	891
Db	568	GGCGCCGATCGCGCACTGGTCTGAGCGAGTACGGCGCCCTGATGTGGACTGGGCGGTG	627
Qy	892	ATGAGTACTACGGCGGCGGCTACGTATCAACGTCTCCGCGGCAATGCGCGGCTTCAACGCC	951
Db	628	CTGACTTGCAGCGCGGCGCACCGTGTGCAATCAACGCGGGTATGCGCGGCTGTGTGCGC	687

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RESULT 7
US-09-252-991A-7330/c
; Sequence 7330, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 7330
; LENGTH: 1575
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7330

```

	Query Match	3.0%:	Score 111.8;	DB 3;	Length 1575;
	Best Local Similarity	51.7%;	Pred. No. 5e-13;		
	Matched 328;	Conservative 0;	Mismatches 277;	Indels 30;	Gaps 2;
QY	323	TCGCGGTGGCGCTACAGAGGGAACAGTCGCGCGCTCGGTGGCGAGCTGAGTGAACAAGGAGG	382		
DB	1571	TGTCTCTTGCTTTGCGGCGCGCTCCGCTGCGCGCGAGAGACCGCTCTGAACAAGCGGCG	1512		
QY	383	ACAAAGCGGTGGACCTGTGTGGCGGCGAGCGCTGTGTGGGGCTTCAAGAGCGTGTCCGGGCTTTGG	442		
DB	1511	ACACCGCGCTGGATCTGTATCTCCACTGGCGCTGTCTCTGTCATGACCATCCCGGCGCTGG	1452		
QY	443	TGTGTCTGTACGGGGGCGCTGTGTGAAGAAAGATGGGGCGGTGAATTCGGCGCTTATATGGCGC	502		
DB	1451	CGCTGTTCTTACGGGGGCAATGGTGTGGAGGAAACGTGCTCTGCATCATATGACAGTCT	1392		
QY	503	TCTACGCTTGCGCGCGCTGTGAGATTTGTCGTGGGTCACTGGGCGCTACAACTGTCTGTTG	562		
DB	1391	TGCGCATACCGGCGCTGATCACCAATTTCTCTGGGTGTCTATATGGCTACAGCCTGGCGTTTCG	1332		
QY	563	GAGAGAAAGCTCTCCCGATCTGGGGGAAAGGCGCGGCGCGCTGAGACCGAGGCGCTTCTTCG	622		
DB	1331	ATACCA-----CGGGATGGAAGAAAGGCGGTCTCTCAACTTCA	1296		
QY	623	TCGGCGCGCGCGCGCTCGGCGAGCGTTCACATACCGGCGCGGACGACGCGCTGGAGACGG	682		

Db 1295 ATTCTTCTGCGGAGCATGACAGACCTTCTTACGCGGTCTACCGCGGACGCTGA 1236
Qy 683 CGGCGGTGAGCGCGCTGTACCCGATGCGACGCTGTGTATTCAGATGCGTGTGCGG 742
Db 1235 CTTCGCGCACCGGCGCTGTCCCGAAGCGTGTATTCACCTTCCAGATGACCTTGCAG 1176
Qy 743 CCATACCTCTCATCTCTGTGCGCGGCTCCCTCTCGGCGCGGACGATCTTCTGCGTGA 802
Db 1175 TCATCATCTCGGCGGTGTGTGTGCGGCTTGGCGGAGCATGAAGTTCGCGGATGC 1116
Qy 803 TGAATCTTGTCCGCTGTGCTGTGCTCACTTCTCTACACCGTCCGCGCTTCTCCCTGTG- 861
Db 1115 TGAATCTTGTATGCGGCTGTGTGTATTCAGCTGTGTCTACCGCGGATGCGACATGTGTGA 1056
Qy 862 -----GCGGCGGCTTCTCTTCTCACTGCGGCGTATCATCTACTGCGGCGGTACTGA 916
Db 1055 GCGGTACCGCGCGCTGTATGTGTGAGTGTGGGCGGTGTGTGACTTGCAGCGGCGGCGTGA 996
Qy 917 TCACAGTCTCCGCGGCGGATGCGCGGCTTACCGCC 951
Db 995 TGCACATCAACGCGGATGTGCGGTGTGTGCGCC 961

RESULT 8

US-09-249-585A-4
; Sequence 4, Application US/09249585A
; Patent No. 6417002
; GENERAL INFORMATION:
; APPLICANT: Horlick, Robert
; TITLE OF INVENTION: METHOD FOR MAINTENANCE AND SELECTION OF EPISOMES
; FILE REFERENCE: 0867/0905
; CURRENT APPLICATION NUMBER: US/09/249,585A
; CURRENT FILING DATE: 1999-02-11
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 1926
; TYPE: DNA
; ORGANISM: Epstein Barr Virus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(1926)
; OTHER INFORMATION: template strand of EBNA-1 DNA
US-09-249-585A-4

Query Match 2.8%; Score 103; DB 3; Length 1926;

Best Local Similarity 51.6%; Pred. No. 3.5e-11;
Matches 235; Conservative 0; Mismatches 220; Indels 0; Gaps 0;

Qy 2919 GTGCTGCGCGGAGCATCCGCTGTATCACCATGATCTCTGACAGCGCTCCAGATC 2978
Db 542 GTCTCTCCCGTCTGCTCTCTCCCGTCTCCCGTCTCCCGTCTCCCGTCTCTCTC 601
Qy 2979 CTGACGCGGTGACAGACCTCTGCGGTCTTCCACACCGAGCGTCCGCGCTCTC 3038
Db 602 CCGGTCTGCTCTCCCGTCTCCCGTCTCCCGTCTCCCGTCTCCCGTCTCTCTC 661
Qy 3039 GCGGCGCTCTGACCGGCTCTTGTGCGGAGCCACCTCTGCAACCTCTTCTCCCGT 3098
Db 662 CTCTCTCCCGTCTCCCGTCTCTCCCGTCTCCCGTCTCTCTCTCTCTCTCTCTC 721
Qy 3099 GCGGACTCTCCGAGGCGCTTCTAAGGCGGCGCGGCGGCGGCGGAGTTGCGCAAGATC 3158
Db 722 CTGCTCTCCCGTCTCTGCTCTCTCCCGTCTCTCCCGTCTCTCCCGTCTCTCTC 781
Qy 3159 GCGGCGGCTCTTCTGCTCTGCTGGAAGTGTGTCTACCTCTCCGATCTGCTCTGCG 3218
Db 782 GTCTCTGCTCTCTCCCGTCTCTCCCGTCTCTCTCTCTCTCTCTCTCTCTCTCTC 841
Qy 3219 ATCAACTCTCTGCTCTGCTCTGCGATGCGGAGCAAGATCTGAGGTGCGGAGCAAGCC 3278
Db 842 CTCTCTCCCGTC 901

Qy 3279 GTTCAAGGAGAGAGGCTTACGCGCTGTGGGCGAGCGGAGATGTATGACACTCAAG 3338
Db 902 CTCTCCGCTCTGCTC 961
Qy 3339 CACGCTCTCGAGCGCGCGCTTGCCTCCCGTCTGCT 3373
Db 962 CCGGTCTGCTCTCACTCTCGGCGCCAGCTCTCT 996

RESULT 9

US-09-130-114-2
; Sequence 2, Application US/09130114
; Patent No. 5976807
; GENERAL INFORMATION:
; APPLICANT: Horlick, Robert A.
; APPLICANT: Damaj, Bassam B.
; APPLICANT: Robbins, Alan K.
; TITLE OF INVENTION: Eukaryotic Cells Stably Expressing Genes
; TITLE OF INVENTION: From Multiple Transfected Episomes
; FILE REFERENCE: 0867/10903US1
; CURRENT APPLICATION NUMBER: US/09/130,114
; CURRENT FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 1931
; TYPE: DNA
; ORGANISM: EBNA
US-09-130-114-2

Query Match 2.8%; Score 103; DB 2; Length 1931;

Best Local Similarity 51.6%; Pred. No. 3.6e-11;
Matches 235; Conservative 0; Mismatches 220; Indels 0; Gaps 0;

Qy 2919 GTGCTGCGCGGAGCATCCGCTGTATCACCATGATCTCTGACAGCGCTCCAGATC 2978
Db 542 GTCTCTCCCGTCTGCTCTCTCTCCCGTCTCCCGTCTCCCGTCTCCCGTCTCTC 601
Qy 2979 CTGACGCGGTGACAGACCTCTGCGGTCTTCCACACCGAGCGTCCGCGCTCTC 3038
Db 602 CCGGTCTGCTCTCCCGTCTCCCGTCTCCCGTCTCCCGTCTCCCGTCTCTCTC 661
Qy 3039 GCGGCGCTCTGACCGGCTCTTGTGCGGAGCCACCTCTGCAACCTCTTCTCCCGT 3098
Db 662 CTCTCTCCCGTCTCTCCCGTCTCTCCCGTCTCTCCCGTCTCTCTCTCTCTCTC 721
Qy 3099 GCGGACTCTCCGAGGCGCTTCTAAGGCGGCGGCGGCGGCGGAGTTGCGCAAGATC 3158
Db 722 CTGCTCTCCCGTCTCTGCTCTCTCCCGTCTCTCCCGTCTCTCCCGTCTCTCTC 781
Qy 3159 GCGGCGGCTCTTGTGCTGTGGAAGTGTGTCTACCTCTCTGATCTGCTCTGCG 3218
Db 782 GTCTCTGCTCTCTCCCGTCTCTCCCGTCTCTCCCGTCTCTCCCGTCTCTCTC 841
Qy 3219 ATCAACTCTCTGCTCTGCTCTGGAAGTGTGTCTACCTCTCTGATCTGCTCTGCG 3278
Db 842 CTCTCTCCCGTC 901
Qy 3279 GTTCAAGGAGAGGCTTACGCGCTGTGGGCGAGCGGAGATGTATGACACTCAAG 3338
Db 902 CTCTCCGCTCTGCTC 961
Qy 3339 CACGCTCTCGAGCGCGCGCTTGCCTCCCGTCTGCT 3373
Db 962 CCGGTCTGCTCTCACTCTCGGCGCCAGCTCTCT 996

RESULT 10

US-09-197-649-7
; Sequence 7, Application US/09197649
; Patent No. 6194550
; GENERAL INFORMATION:
; APPLICANT: Gold, Larry

```
APPLICANT: Tuerk, Craig
APPLICANT: Pithnow, David
APPLICANT: Smith, Jonathan D.
TITLE OF INVENTION: Systematic Polypeptide Evolution by Reverse Translation
FILE REFERENCE: NEX02/C1-CON
CURRENT APPLICATION NUMBER: US/09/197,649
CURRENT FILING DATE: 1998-11-23
EARLIER APPLICATION NUMBER: 07/829,461
EARLIER FILING DATE: 1992-01-31
EARLIER APPLICATION NUMBER: 07/739,055
EARLIER FILING DATE: 1991-08-01
EARLIER APPLICATION NUMBER: 07/561,968
EARLIER FILING DATE: 1990-08-02
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENGTH: 390
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Sequence
OTHER INFORMATION: having a 120 repeat of ACG flanked by fixed
OTHER INFORMATION: fragments having NcoI restriction sites.
US-09-197-649-7
```

```
Query Match 2.6% Score 97.2; DB 3; Length 390;
Best Local Similarity 53.4%; Pred. No. 2.5e-10;
Matches 204; Conservative 0; Mismatches 178; Indels 0; Gaps 0;
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QY 2987 CGTCGACGACACCTCGGCGCTTTCACACCGCGCTCGCGGCTTCTCGGCGGCTT 3046
DB 5 CATGGAACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 64
QY 3047 CCTCAGCGGCTTCTTCCGAGCCCACTCTGCAACTCTTCTCCCGTGGCGACTC 3106
DB 65 CGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 124
QY 3107 CGGGGCGGCTTCTACGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3166
DB 125 CGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 184
QY 3167 CCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3226
DB 185 CGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 244
QY 3227 CCTGCTCCGCTCCGATGCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3286
DB 245 CGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 304
QY 3287 CGAGGAGGCTTACGCGCTCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3346
DB 305 CGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 364
QY 3347 CGACGCGCGCGCTTGCCTCCCGCTC 3368
DB 365 CGACGCGCATGTTGCATGCTC 386
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```
RESULT 11
US-09-252-991A-7285
Sequence 7285, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
```

```
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 7285
LENGTH: 987
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7285
```

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Query Match 2.5% Score 91.6; DB 3; Length 987;
Best Local Similarity 59.7%; Pred. No. 5.6e-09;
Matches 154; Conservative 0; Mismatches 104; Indels 0; Gaps 0;
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```
QY 1269 GTTCCCGCGCAACATATAGTTTACAGCGGCGGCGAGGCTGTGTGATGGGTTG 1328
DB 130 GATGCGCGCGCAACATCTCGGTACACCTGTGTGCGGCGCGCAATGTGTGATCGCTG 189
QY 1329 GCGAGGTTTCAACGGCGCGGCTCTTACGCGCGCAACTCCGTGCTTATAGCCGCT 1388
DB 190 GTTGGTTTCAACGGCGGTTCCGCGCGCGCGCAACGGCGCGCGGAGATGGCCATGCT 249
QY 1389 CAACCAACATCTGACCGCGCATGAGCTCATGCTGATGATGCTCGATGCTT 1448
DB 250 GGTGACCGCATGCGCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 309
QY 1449 CTTCAAGAACCTTCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1508
DB 310 CCACGCGAAGCGGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCAT 369
QY 1509 CACCCCGCTCGAGGTAC 1526
DB 370 CACCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 387
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```
RESULT 12
US-09-103-840A-2
Sequence 2, Application US/09103840A
Patent No. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 4403765
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
FEATURE:
OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence
OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2
```

```
Query Match 2.4% Score 90; DB 3; Length 4403765;
Best Local Similarity 51.5%; Pred. No. 8.2e-07;
Matches 207; Conservative 0; Mismatches 195; Indels 0; Gaps 0;
```

```
QY 3006 GTCTTCCACACCCAGGCGGTGCGCGGCTCTCTCGGCGGCGCTTCTACCGGCTTTCGCC 3065
DB 1189045 GCGGCGCGACCGCGCGGTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1189104
QY 3066 GAGCCACCTCTTGCACCTTCTCTCCCGTCCGCACTCCCGGCGCGCGCTTCTACGCG 3125
DB 1189105 GTTACCACTATGTGGGGTTGAGCCGAGTGGCGCGCGCGCGCGCGCGCGCGCGCG 1189164
QY 3126 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3185
DB 1189165 GCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1189224
```

QY 3186 AACGTGTGTGATCACTTCCCTCATCTGCTGCGCATCACTCTGCTCCGCTCCGCGATG 3245
DB 1189225 GTGGCCGCGACACCCGCTACCTTATCCGGGTGGCCACGACATGTTGCGCGCC 1189284
QY 3246 CCCGACGACAAAGTCCAGGTCCGCGACGACGCGCTCCACGCGAGAGAGCGCTACGCGCTC 3305
DB 1189285 GGGGCGCGCGCGCGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCTGCGCGCGCTGCGCGC 1189344
QY 3306 TGGGCGGACGCGGAGATGTAAGACGTCACCAAGACGCGCTCCGACGCGCGCGCTGCGCGCC 3365
DB 1189345 GAACAGCAGCGCGCGCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCTGCGCGCGC 1189404
QY 3366 GTGCTGTATGATGATCACTATTAATGATGCTGCTGAC 3407
DB 1189405 GGTGCGCGCTGCTGACCGAATTGGCGCGCGCTGCGCGAC 1189446

RESULT 13

US-09-103-840A-1
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match 2.4%; Score 90; DB 3; Length 4411529;
Best Local Similarity 51.5%; Pred. No. 8.2e-07;
Matches 207; Conservative 0; Mismatches 195; Indels 0; Gaps 0;

QY 3006 GTCTTCACACCCACGCGCTGCGCGCTCTGCGCGCTCTCTCAACGCGCTCTTCCGCC 3065
DB 1189019 GCGGCGCGACCCCGCGTGCCTGCGCGCGCGCGCTGCGCGCGCGCGCGCGCGCGCGC 1189078
QY 3066 GAGCCCACTCTGCAACTCTTCTCTCCCGTGGCGGACCTCCGCGCGCGCTTCTACGCGC 3125
DB 1189079 GTTACCACTAGTGGCGCGCTTGAAGCCGCGTGGCGCGCTGCGCGCGCGCGCGCGCGC 1189138
QY 3126 GGGGCGCGCGCGCGCGCTGCGCGCGCGCGCGCGCGCGCTTCTGCGCTGCGCTGCG 3185
DB 1189139 GCGGCGCGCGCGCTGC 1189198
QY 3186 AACGTGTGTGATCACTTCCCTCATCTGCTGCGCATCACTCTGCTCCGCTCCGCGATG 3245
DB 1189199 GTGGCGCGCGCGCGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 1189258
QY 3246 CCCGACGACAAAGTCCAGGTCCGCGACGACGCGCTCCACGCGAGAGCGCTTACGCGCTC 3305
DB 1189259 GGGGCGCGCGCGCGCGCGCTTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 1189318
QY 3306 TGGGCGGACGCGGAGATGTAAGACGTCACCAAGACGCGCTCCGACGCGCGCGCTGCGCGCC 3365
DB 1189319 GAACAGCAGCGCGCGCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTGCGCGC 1189378
QY 3366 GTGCTGTATGATGATCACTATTAATGATGCTGCTGAC 3407
DB 1189379 GGTGCGCGCTGCTGACCGAATTGGCGCGCGCTGCGCGAC 1189420

RESULT 14

US-09-023-173-4
; Sequence 4, Application US/09023173
; Patent No. 6066781
; GENERAL INFORMATION:
; APPLICANT: Sulliff, Thomas D.
; APPLICANT: Rodriguez, Raymond L.
; TITLE OF INVENTION: Production of Mature Proteins
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESS: Dehlinger & Associates
; STREET: 350 Cambridge Ave., Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA

ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,173
; FILING DATE: 13-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/038,168
; FILING DATE: 13-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Petlichory, Joanne R
; REGISTRATION NUMBER: P42995
; REFERENCE/DOCKET NUMBER: 0665-0007.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-0880
; TELEFAX: 650-324-0960
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1140 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: codon-optimized Ramy3D signal-prosutilisin BPN'
US-09-023-173-4

Query Match 2.4%; Score 89.8; DB 3; Length 1140;
Best Local Similarity 52.2%; Pred. No. 1.4e-08;
Matches 199; Conservative 0; Mismatches 182; Indels 0; Gaps 0;

QY 2993 CGACACCTCGGCGCTTCCACACCGACGCGCTGCGCGCTTCTGCGCGCGCTCTCAAC 3052
DB 465 CGAGACCAACCGCTTCCAGACCAACCAAGCATGGACCCACGTCGCGCGCACCTTCGC 524
QY 3053 CGGCTCTTGGCGGACCACTCTGCAACTCTTCTCTCCCGTGGCGGCGCGCGCGCGCGG 3112
DB 525 CGGCTTCAACCAAGCATGGCGCTCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 584
QY 3113 CGGCTTCAACGC 3172
DB 585 CAAGTACTTGGC 644
QY 3173 CGTGTGCGCTGGAAAGTGTGTGTCACCTCTCATCTGCTGCGCATCACTCTCTGCT 3232
DB 645 GGGCATTCGCAACCAATGAGTATCACTAGACCTTGGCGCGCGCGCGCGCGCGCGCGC 704
QY 3233 CCGGCTTCGC 3292
DB 705 CGGCTTCAAGC 764
QY 3293 GGCCTACGCGCTTGGGCGGACGCGCGAGATGTAAGACGTCACCAACGCGCGCTTCGACGC 3352

Db 765 CGGCAACGAGGCGACCGAGCGAGCAGACACCGTGGCTACCGGCGCAAGTACCGAG 824

Job time : 1213 secs

QY 3353 CGCCGTTGCCCGCTGTGTGT 3373
Db 825 GGTCAATCGCGCTGGCGCGCT 845

RESULT 15

US-09-974-300-5249/C
; Sequence 5249, Application US/09974300
; Patent No. 7018794
; GENERAL INFORMATION:
; APPLICANT: Berka, Randy M.
; APPLICANT: Clausen, Ib Groth
; TITLE OF INVENTION: Method For Monitoring Multiple Gene
; TITLE OF INVENTION: Expression
; FILE REFERENCE: 10085.500-US
; CURRENT APPLICATION NUMBER: US/09/974,300
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 09/580,598
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/279,526
; NUMBER OF SEQ ID NOS: 8481
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5249
; LENGTH: 863
; TYPE: DNA
; ORGANISM: Bacillus clausii
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(863)
; OTHER INFORMATION: n = A,T,C or G
US-09-974-300-5249

Query Match 2.4%; Score 89; DB 5; Length 863;
Best Local Similarity 51.3%; Pred. No. 1.8e-08;
Matches 231; Conservative 0; Mismatches 216; Indels 3; Gaps 1;

QY 2923 TGGCCGCGAGCATCCCGGTGTACACCATGATGCTCTCCACAGCGCTCCAGATCTTGC 2982
Db 575 TCAGCGTCCGAATCCGCATCCGCATCGGCGTCCGATCCGCATCGGCATCGGCATCGCG 516
QY 2983 AGCGCGTCGACGACACCTCGGCGCTTTCACACCCAGCGCGCGCGCTTCTCGCGCG 3042
Db 515 TCAGCATCAGCGTCCGCATCGGCGTGGCATCGGCATCGGCATCGGCGCTCCGAATCCGA 456
QY 3043 GCCTCTCAACGCGCTCTTCGCGAGCCGACCCCTCTGCAACTTCTTCCCGTCCCG 3102
Db 455 TCGCATCGGCGTCCGCATCCGCATCGCATCGGCATCGGCATCGGCATCGAGGTCAGCG 396
QY 3103 ACTCCCGGGGCGCTTCTACGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3162
Db 395 TCGGCAATCGGCGTCCGCATCCGCATCGCATCGCATCGCGCTCCGCTCCGCGATCGCG 336
QY 3163 GCGGCGCTTTCGCTCGGCTGAGCGTGTGACCTCCCTCATCTGCTGCGCCATCA 3222
Db 335 TCGCATCCGCATCCGCGTCCG---CGTGGCATTCGCGTCAAGCATCAAGCGTCCGATCA 279
QY 3223 ACCTCTCTGCTCCGCTCCGATCCGAGCCGAGCAAGCTCGAGGTGGCGAGCGCGCTCC 3282
Db 278 GCGTCCGCGTCCGCATCGGCATCGCGGTGCGGCGTCCGATCCGCGTCCGCGATCGCG 219
QY 3283 AGGCGAGAGAGCGCTTACGCGCTTGGGGGAGCGCGAGATGTACAGCTACCAAGACAG 3342
Db 218 GGTTCAGCATCAGCATCAAGCGTCCGCGTCTGCGTCCGATCCGATCCGATCCGATCCG 159
QY 3343 GCTCCGACGCGCGCTTGGCGCGCGCTGATCG 3372
Db 158 GCATCGCGCTCAGCGTCCGCGATCCGATCC 129

Search completed: July 23, 2006, 15:40:17

Db 122 GAACAAAGGGGCGAACAGCTGGGACGCTGGCGGGAGACGCTGGTGGGGCTCAAGACCT 181
Qy 432 GCGGGCTTGTGTGTCTGTACCGCGGCGGTGTGAAGAAAGTGGCGGTGAACCTGGC 491
Db 182 GCGGGCTTGTGTGTCTGTACCGCGGCGGTGTGAAGAAAGTGGCGGTGAACCTGGC 241
Qy 492 GTTCAATGGGCTCTAGGCTTGGCGGCGGTGTGAAGTGGCGGTGAACCTGGCGGCA 551
Db 242 GTTCAATGGGCTCTAGGCTTGGCGGCGGTGTGAAGTGGCGGTGAACCTGGCGGCA 301
Qy 552 CATGTCTGGGAGAGAACTCTCCGATCTGGGAGAAAGCGCGGCGGTGAACCA 611
Db 302 CATGTCTGGGAGAGAACTCTCCGATCTGGGAGAAAGCGCGGCGGTGAACCA 361
Qy 612 GGGGCTCTGT 671
Db 362 GGGGCTCTGT 421
Qy 672 CGTGAAGAGGGGCGGT 731
Db 422 CGTGAAGAGGGGCGGT 481
Qy 732 CGTGTTCGCGGCATCACCTCATCTCGTCGCGGCTCTCTCGCGCGATGAGCTT 791
Db 482 CGTGTTCGCGGCATCACCTCATCTCGTCGCGGCTCTCTCGCGCGATGAGCTT 541
Qy 792 CCGCGCTGT 851
Db 542 CCGCGCTGT 601
Qy 852 CTCCTCTGGGGGCGGCTTCTCTCTCACTGGGGCGGTGTGTGTGTGTGTGTGTGTGTGTGT 911
Db 602 CTCCTCTGGGGGCGGCTTCTCTCTCACTGGGGCGGTGTGTGTGTGTGTGTGTGTGTGTGT 661
Qy 912 CGTCAATCAAGTCTCGCGCGGATCGCGGCTTCAACCGCGCTTACTGGGCTCGTACTA 970
Db 662 CGTCAATCAAGTCTCGCGCGGATCGCGGCTTCAACCGCGCTTACTGGGCTCGTACTA 720

RESULT 2

US-10-033-109-13
; Sequence 13, Application US/10033109
; Publication No. US20020142390A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Stephen M.
; APPLICANT: Rafaleki, J. Antoni
; APPLICANT: Sakai, Hajime
; TITLE OF INVENTION: Nitrogen Transport Metabolism
; FILE REFERENCE: BB-1210
; CURRENT APPLICATION NUMBER: US/10/033,109
; PRIORITY FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/384,625
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/098,248
; PRIOR FILING DATE: EARLIER FILING DATE: 28 August 1998
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 13
; LENGTH: 1656
; TYPE: DNA
; ORGANISM: Trifolium aestivum
US-10-033-109-13

Query Match 14.4%; Score 529.2; DB 6; Length 1656;
Best Local Similarity 86.9%; Pred. No. 9.3e-94;
Matches 582; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

Qy 306 GTCTGCGGAGAGGT 365
Db 83 GTCTGCGGAGAGGT 142
Qy 366 CTGGCTGAACAAGGGGAGCAACGCTGTGACGCTGTGTGCGGACGCTGTGTGGGCTGTGA 425

Db 143 CTGGCTGAACAAGGGGAGCAACGCTGTGACGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 202
Qy 426 GAGCTGTCCGGGCTTGT 485
Db 203 GAGCTGTCCGGGCAAGT 262
Qy 486 CTGGGCTTCAATGGGCTCTAGGCTTGGCGGCGGTGTGAATGTGGTGGTCACTGGGCG 545
Db 263 CTGGGCTTCAATGGGCTCTAGGCTTGGCGGCGGTGTGAATGTGGTGGTCACTGGGCG 322
Qy 546 GTACAACATGTCTGT 605
Db 323 GTACAACATGTCTGT 382
Qy 606 GGAACAGAGGCTCTCTGT 665
Db 383 GGAACAGAGGCTCTCTGT 442
Qy 666 GGGCAGCGGTGAAGAGGGGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 725
Db 443 GGGCAGCGGTGAAGAGGGGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 502
Qy 726 CCAAGT 785
Db 503 CCAAGT 562
Qy 786 GAGCTTCTCGGCTGT 845
Db 563 GAGCTTCTCGGCTGT 622
Qy 846 GCGCTTCTCGGCTGT 905
Db 623 GCGCTTCTCGGCTGT 682
Qy 906 CCGCTACGATCAACGATCTCGCGCGGATCGCGGCTTCAACCGCGCTTACTGGGCTCG 965
Db 683 CCGCTACGATCAACGATCTCGCGCGGATCGCGGCTTCAACCGCGCTTACTGGGCTCG 742
Qy 966 TACTTACAGC 975
Db 743 GCCAAGAGAC 752

RESULT 3

US-11-012-668-13
; Sequence 13, Application US/11012668
; Publication No. US20060010512A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Stephen M.
; APPLICANT: Rafaleki, J. Antoni
; TITLE OF INVENTION: Nitrogen Transport Metabolism
; FILE REFERENCE: BB-1210
; CURRENT APPLICATION NUMBER: US/11/012,668
; PRIORITY FILING DATE: 2004-12-15
; PRIOR APPLICATION NUMBER: 60/098,248
; PRIOR FILING DATE: 28 August 1998
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 13
; LENGTH: 1656
; TYPE: DNA
; ORGANISM: Trifolium aestivum
US-11-012-668-13

Query Match 14.4%; Score 529.2; DB 16; Length 1656;
Best Local Similarity 86.9%; Pred. No. 9.3e-94;
Matches 582; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

Qy 306 GTCTGCGGAGAGGT 365
Db 83 GTCTGCGGAGAGGT 142

Db 113 AGAGGAGGTATATACGTAGGACCGCCGGCCGGCAACTTAACTTAATGTCGTCGTCGG 172

Qy 315 GACGGTGTGTCGCCGTGACGTACCAAGGGAACAAGTCGGCGTGGCGGACTGGCTGAA 374

Db 173 GACGACGATGCGCGTGGCGTACGAG-----ACGTGGCGTCTCTCCGAGTGGCTGAA 226

Qy 375 CAAGGGGGAACAACGCGTGGCACTGGTGGCCGGCAACGCTGGTGGGGCTGGAGACGGGCC 434

Db 227 CAAGGGCGCAACAACGGTGGCACTGAACGGCCGGCAACGCTGGTGGGGCTGGAGACTTCC 286

Qy 435 GGGCTTGGTGGTGGTGGTGAACGGCGGCTGGTGAAGAAAGTGGCGGTGAATCTGGCGTT 494

Db 287 GGGTCTGGTGGTGGTGGTGAACGGCGGCGGTGAAGAAAGTGGCGGTGAATCTGGCGTT 346

Qy 495 CATGGCGCTTACGCGCTTGGCGCGCGGTGGATCTGCTGGGTGAACCTGGCGGTACAAAT 554

Db 347 CATGGCGCTTACGCGCGCTTGGCGCGGTGGATCTGCTGGGTGAACCTGGCGGTACAAAT 406

Qy 555 GTCGTTCCGGGGGAAGATCTCCGATCTGGGGGAAGGGCGCGCGGTGAACCGAGG 614

Db 407 GTCCTTCCGCGCAAGCTGCTGGCTGGGGGAAGGGCGCGCGGTGAACCGAGG 466

Qy 615 CTTCTCTGTCGAGCGCGCGCGCTGGCGCGCAAGCTGCACTAACCGCGCGCAAGCGT 674

Db 467 CTGGCTGGTGGGGCAAGCGCGCGCTCCCGCGCAAGCGCGCAACTTGGCGAGCGCGCGCT 526

Qy 675 GGAGACGAGCGCGCGTGGAGCCCGCTGTACCCGATGGCGAGCGTGTACTTCCAGTGGCT 734

Db 527 GGAGACCCCGCGCGCGAGCCCGCTGTACCCGATGGCGAGCGTGTACTTCCAGTGGCT 586

Qy 735 GTTCCCGCGCAACACCCCTATCCTCGTGGCGCGCGCTCCCTCGTGGCGCGATGAGCTTCT 794

Db 587 GTTCCCGCGCAACACCCCTATCCTCGTGGCGCGCGCTCCCTCGTGGCGCGATGAGCTTCT 646

Qy 795 CGCTCGATGATCTTCTGTCGCGCTGTGAGCTTCTCTCAACACCGTGGCGCGCTTCTC 854

Db 647 CGCGGAGATGCTGTCGTCGCGCTGTGAGCTTCTCTCAACACCGTGGCGCGCTTCTC 706

Qy 855 CCTTGGGGCGCGCGCTTCTCTTCACTGGGGCGTATGATTAATGCGCGGCTTACGT 914

Db 707 CGTCTGGGGCGCGCGGTTCTCTTCAAGGGGGCGTATGATTAATGCGCGGCTTACGT 766

Qy 915 CATCCACGCTTCCGCGCGGATGCGCGGCTTCAACCGCGCTTACTTGGGT 962

Db 767 CATCCACCTTCCGCTGGCTTGGCGGGTTCAACGAGCCTTAATGGGT 814

RESULT 5
US-10-437-963-44521
; Sequence 44521, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Bardazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966

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;
; LENGTH: 1497
;
; TYPE: DNA
;
; ORGANISM: Oryza sativa
;
; FEATURE:
;
; OTHER INFORMATION: Clone ID: PAT_MRT4530_47574C.1

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US-10-437-963-44521

12.3%; Score 453; DB 8; Length 1497;

Best Local Similarity 81.8%; Pred. No. 9.8e-79;

Matches 554; Conservative 0; Mismatches 105; Indels 18; Gaps 2;

OY	301	ATGTGTCGTGGAGCGACGGTGGGCGCTGGGCGCTACCAAGAGGAAACAAGTCGAGGTCGATG	360
Db	1	ATGTGCGGGAGACGCGCTTCAACATATCTGGGTGGCTACCAAGCG---TCGGGAAATGGCGGTG	57
OY	361	GGGAGCTGGCTGAACAAAGGAGGAGCAACGCGGTGGACGTGGTGGCGCGACCTGTGGGG	420
Db	58	CCGGAGTGGCTGAACAAAGGAGGCACAACGCGTGGCAATATCTCGGCGACGCTGTGGGG	117
OY	421	CTGCAGAGCGTCCCGGGCTTGGTGGGTCTGTACGAGGGGGGTGGTGAAGAAAGTGGGGG	480
Db	118	ATGCAGAGGCTCCGGGGCTGGGTGATCTGTACGGGAGCATCTGAAGAAAGTGGGGG	177
OY	481	GTGAAGCTGGCGCTTACATGCGCGCTCTAAGCGCTTCCGCGCGGTGTGAATCTTCTGGGTCA	540
Db	178	GTGAAGCTGGCGCTTACATGCGCGCTCTAAGCGCTTCCGCGCGGTGTGGCTGTGGGTCA	237
OY	541	TGGGCGTACACATATCTCTCTTCCGGGAGAAAGCTCTTCCCATCTTGGGGGAAAGCGCGGG	600
Db	238	TGGGCGTACAAACATATCTCTCTTCCGGGCAACAAGCTCTTCCCTTCTTGGGGCAAGGCGCGGG	297
OY	601	GCGCTGAGACAGAGGCTCTCTCTGTGGGCGCGCGCGCGCTGGCGCGGACGATCACT-----	655
Db	298	GCGCTGGGCGACAGAGCTTCTCTCTCTGGGCGAAGGCGGTGTCCGAGAGACGAGTCTTAC	357
OY	656	-----ACCGCGCCGACGCGACGCGTGGAGACGCGCGCGGTGGAGCGCGCTGTACCGG	705
Db	358	AAAGGCGGCGGCGCGCGCCACACGCGGTGGTGGAGACGCGATGGGTGAACCGCGCTACCGG	417
OY	706	ATGGCGACGCGGTGTACTTCCAGTGCAGTGTGGCGGCATCAACCTCATCTCTGTGCGC	765
Db	418	ATGGCGACCATGTGTACTTCCAGTGCAGTGTGTTCGCGGCATCAAGCTCATCTCTGTGCGC	477
OY	766	GGCTCCCTCTCTGGCGCCGATGAGCTTCTCTCGCTGTGAATGTCCTTGGTCCGCGCTGTGGCTC	825
Db	478	GGCTCGCTCTGGGGCGGATGAACATCAAGGCGCTGTGATGTCTTGTGTCGCGCTGTGGCTC	537
OY	826	ACCTTCTCCTTACACCGTGGGCGCTTCTCTCTCTGGGGGCGGCGGCTTCCCTTCCACTGG	885
Db	538	ACCTTCTCTTACACCGTGGGCGCTTCTCTCTCTGTGGGGCGGCGGCTTCTCTTCCACTGG	597
OY	886	GCGCTCATCGACTATGCGCGCGGCTACGTCATCCAGTCTCCGCGCGGCATCGCGCGCTTC	945
Db	598	GCGGTCATGACTACTCCGGCGGCTAGTCATCCACTCTCTGTGGGTGTGCGCGGCTTC	657
OY	946	ACCGCGCTTACTGGGT	962
Db	658	ACCGCGCGTACTGGGT	674

RESULT 6
US-10-425-115-73446

```

; ORGANISM: Zea mays
;
; FEATURE:
;
; OTHER INFORMATION: Clone ID: MRT4577_166983C.1
US-10-425-115-73446

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Match	11.4%	Score 419;	DB 9;	Length 2130;
-------	-------	------------	-------	--------------

Best Local Similarity 79.8%; Pred. No. 6.1e-72.

Matches 494; Conservative 0; Mismatches 125; Indels 0; Gaps 0;

OY	344	ACAGTCGGAGCTCGGTGGCGGACCTGCGTGAACAAAGGGGACAACCGCGTGGACGCTGATGG	403
Db	351	AGAGTCGTGGGGCTCGCGGACCTGCGTGAACAAAGGAGACAAATCGCTGGCAGATGAGT	410
OY	404	CGGCGACGCTGTGGGGGCTGCAGAGCGTCCGGGCTTGGTGTGCTGATGAGGCGGCGTGG	463
Db	411	CCGCGACGCTGTGGGGCTGCAGAGCAATGCCGGGCTGTGATCCTGTACGGGACGATCG	470
OY	464	TGAAGAAAGATGGGCGGTGAACCTCGCGCTTCAATGGCGCTCTAAGCGCTTCCCGCGGTG	523
Db	471	TGAAGAAAGATGGGCGCATCAACTCGGGTTCATAGCGCTGTACGCCCTTCCGCGCGTCT	530
OY	524	GGATCTGCTGGGTCAACCTGGGCGGTAAACAATGTGCTGGGGAGAAAGCTCCTCCGATCT	583
Db	531	GGCTCTGTGGGTGTGTGTGGGCTCAACAACATGTGTTGGGGACCGGCTGTGCCCTTCT	590
OY	584	GGGGGAAAGCGCGGCGCGGCGCTTGAACAAGGCGCTCTCTGTGGCGCGCGCGGCTGGCGG	643
Db	591	GGGGCAAGAGCGAGGCGCGGCGCTCGGGGCGGCGCTTCTGTGTGGCGGAGTCCAGGCTCAAGG	650
OY	644	CGAGGCTCACTAACCGGCGCGACGCGGAGCGTGAAGACGCGCGGCTGAGCGCGCTGATCC	703
Db	651	CCACCGCGCTGGCGGTACCGGCAAGGGTGCCTGAGGCGGAATGTCTCAACCCCTTCTAAC	710
OY	704	CGATGGCGACGGTGGTGTACTTCCAGTGCAGTGTTCGCCGCATCAACCTCATCTCTGTGG	763
Db	711	CGGCGGCAACATGGGTATCTTCCAGTGCAGTGTTCGCCGAGCATCAACGTCATCATCTCG	770
OY	764	CCGGTCTCCTCTCTGGGCGCGCATGAGCTTCTCGGCTGGAATGATCTTTCCTCCGCGCTGGC	823
Db	771	CCGGTCTCCTCTGGGCGCGCATGGAACATCAAGGCGCTGATGAGCTTCTGTCCGCTCTGGA	830
OY	824	TCACTTCTTCCTAACCGGTGCGGCGCTTCTCCTCTGGGCGGCGGCTTCTCTTCCACT	883
Db	831	TCACTTCTTCTAACCGGTCTTCGCGCTTCTGCTCTGGGGCGGCGGCTTCTCTTCCAGT	890
OY	884	GGGGGTCATGCACTACTGCGGCGGCTTACGTCATCAAGTCTCGGCGGACATGCGCGCT	943
Db	891	GGGGGTCATGCACTACTCGGCGGCTTACGTCATCAAGTCTCTCTCGGGAATGCGCGGCC	950
OY	944	TCAACCGCGCTTACTGGGT 962	
Db	951	TCAACCGCGCTTACTGGGT 969	

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RESULT 6
US-10-425-115-73446
; Sequence 73446, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 73446
; LENGTH: 2130
; TYPE: DNA

RESULT 7
US-10-425-114-27103
; Sequence 27103, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 27103
; LENGTH: 1664

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TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: LIB4721-021-A4_FLI
US-10-425-114-27103

Query Match 11.4%; Score 417.4; DB 8; Length 1664;
Best Local Similarity 79.6%; Pred. No. 1.1e-71;
Matches 493; Conservative 0; Mismatches 126; Indels 0; Gaps 0;

344 ACACGTCGCGCTGCTGCGGCACTGAGTAAACAGGAGGACAACGCGTGCAGCTGCTG 403
121 AAGAGCTCGTCCGCGTCCGCGCACTGCTGAACAAGGCGCAATGCTGCGAGATGACGT 180
404 CGCGCAACGCTGCTGCGGCTGCAAGAGCTCCGCGCTTGTGTGCTGTAACGCGCGCTG 463
181 CGCGCAACGCTGCTGCGGCTGCAAGAGCATGCCGCGTGTGATCTGTAACGCGAGCATG 240
464 TGAAGAAAGAGTGGCGGCTGAACCTGCGCTTCAATGCGCTTCAACGCTTCCGCGCTG 523
241 TGAAGAAAGAGTGGCGGCTGAACCTGCGCTTCAATGCGCTTCAACGCTTCCGCGCTG 300
524 GATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 583
301 GCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
584 GGGGGAAGGCG 643
361 GGGGGAAGGCG 420
644 GAGCGTCACTACCG 703
421 CACCG 480
704 CGATGCG 763
481 CG 540
764 CG 823
541 CG 600
824 TCACCTTCTCTCAACACCGTTCGCGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 883
601 TCACCTTCTCTCAACACCGTTCGCGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 660
884 GGGGCGCTACATCACTACGCGCGCGCTACGCTACGCTACGCTACGCTACGCTACGCT 943
661 GGGGCGCTACATCACTACGCGCGCGCTACGCTACGCTACGCTACGCTACGCTACGCT 720
944 TCACCGCGCGCTTACTGGGT 962
721 TCACCGCGCGCTTACTGGGT 739

RESULT 8
US-10-033-109-9
Sequence 9, Application US/10033109
Publication No. US20020142390A1
GENERAL INFORMATION:
APPLICANT: Allen, Stephen M.
APPLICANT: Rafalski, J. Antoni
APPLICANT: Sakai, Hajime
TITLE OF INVENTION: Nitrogen Transport Metabolism
FILE REFERENCE: BB-1210
CURRENT APPLICATION NUMBER: US/10/033,109
PRIOR FILING DATE: 2001-12-28
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/384,625
PRIOR FILING DATE: EARLIER FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/098,248
PRIOR FILING DATE: EARLIER FILING DATE: 28 August 1998
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Microsoft Office 97

SEQ ID NO 9
LENGTH: 1883
TYPE: DNA
ORGANISM: Oryza sativa
US-10-033-109-9

Query Match 10.6%; Score 389.2; DB 6; Length 1883;
Best Local Similarity 74.0%; Pred. No. 4.4e-66;
Matches 493; Conservative 0; Mismatches 173; Indels 0; Gaps 0;

297 GAAATGTCGTCGTCGCGGCAAGGTCGCTGCGCTGCTGCTGCTGCTGCTGCTGCTG 356
74 GAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 133
357 GGTGCGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 416
134 GGTGCGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 193
417 GGGGCGGCAAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 476
194 CGGCGCTCACTGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 253
477 GCGGCTGATCTGCGGCTTCAATGCGCTTCAATGCGCTTCAATGCGCTTCAATGCG 536
254 GCGGCTGATCTGCGGCTTCAATGCGCTTCAATGCGCTTCAATGCGCTTCAATGCG 313
537 CACTGCGGCTGCAACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 596
314 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 373
597 GCGGCGGCTGCAACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 656
374 GCGGCGGCTGCAACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 433
657 CCGCGCGCAAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 716
434 CCGGCGGCAAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 493
717 GGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 776
494 GGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 553
777 CCGCGCGCAAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 836
554 CCGGCGGCAAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 613
837 CACGCTGCGGCTTCT 896
614 CACGCTGCGGCTTCT 673
897 CTACTGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 956
674 CTACTGCGGCGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 733
957 CTGGGT 962
734 CTGGGT 739

RESULT 9
US-11-012-668-9
Sequence 9, Application US/11012668
Publication No. US2006010512A1
GENERAL INFORMATION:
APPLICANT: Allen, Stephen M.
APPLICANT: Rafalski, J. Antoni
APPLICANT: Sakai, Hajime
TITLE OF INVENTION: Nitrogen Transport Metabolism
FILE REFERENCE: BB-1210
CURRENT APPLICATION NUMBER: US/11/012,668
PRIOR FILING DATE: 2004-12-15
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/098,248
PRIOR FILING DATE: EARLIER FILING DATE: 28 August 1998
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Microsoft Office 97

```

; SOFTWARE: Microsoft Office 97
; SEQ ID NO 9
; LENGTH: 1863
; TYPE: DNA
; ORGANISM: Oryza sativa
; US-11-012-668-9

```

Query Match	10.6%	Score 389.2;	DB 16;	Length 1883;
Best Local Similarity	74.0%	Pred. No. 4.4e-66;		
Matches 493; Conservative	0;	Mismatches 173;	Indels 0;	Gaps 0;

Qy	297	GAAGATGTCGTCGTCGGCACAGTGAGTGCCTGGCTGTACACAGGGGAACAAGTCGGAGTC	356
Db	74	GAAGAAGTGAATGATGCGCTCCGCCAACCCGGCCGGGGCCGTACATGCGCCGCCCAACCGGC	133
Qy	357	GGTGGCGGACTGGCTGAACAAGGGGGAACAAGCGGTGGCAAGTGGTGGCGCGACGCTGGT	416
Db	134	GGTGCGGGAGTGTCTTAMACACGGGGGACAACGGGTGGCAAGCTCGCGGGCGGAGGTTTCGT	193
Qy	417	GGGGCTGCAGAGCGTGCCTGGGGCTTGGTGGTGTATACGGCGGGCGGTGGTGAAGAAGAGTGG	476
Db	194	CGGGCTTTCACATCGATTCCTGGGCTGGGTGGTGTCTGTACGGCAGCATCGTGAAGAAAGATG	255
Qy	477	GGCGGTGAATCGGCGGCTTATGGCGCTTACGCCCTTCGCGCGCGGTGGATCTGCTGGGT	536
Db	254	GGCGGTCACTCGGCTTATGGCGCTGTACCGGTACCGGTCAACGCTCATCGTGGGT	313
Qy	537	CACCTGGGCGTACAAATGTCTGTGGGGGAAGAAGCTCTCCCGATTTGGGGGAAGCGCG	596
Db	314	GCTGGTCGGTTTCGATGAGCGCTTCGGCGAACCGCTGCTCCGTTCTGGGGGAAGGCCGG	373
Qy	597	GCGGCGCTGGAACAAGGCGCTCTCGTCGGCGCGCGCGCGCTGCGCGGACGATCACTA	656
Db	374	CGGGCGCTGAACGGAAGGGTCTCGTGGCGCGCGGTGGTGGTCCGGCCACGGGCACTA	433
Qy	657	CCGGCGCCGACGCGACGCTGGAGACCGCGCGGTGAGCCGCTGTACCCGATGGGGAACGCT	716
Db	434	CGGAAGAGACGGCGCCCTGGAGTGGCGCGACACGAGCGTTTCTAACCGGAGAGGTCAT	493
Qy	717	GGTGTACTTCAGTGGCGTGTGCACGCATTCACCTCACTCGTGGCGGCTCCCTCT	776
Db	494	GGTGTCTTCCATTTGAGACTCGCCGCATCAAGCTGTGTGTCTCGCGGGTGGCTCT	555
Qy	777	CGCGCCGATGACTTCCGCTGATGATCTTCTCCGCTTGGCTACCTTCTCTTA	836
Db	554	CGGAGGATATAMCATCAAGCGGTGGATGGCTTCACTCGCTCTGGCTCTTCTCTTA	613
Qy	837	CACCGTGGGCGCTTCCCTCGCGGGGGCGGCGGCTTCCCTTCACTGAGGGGGTCATGA	896
Db	614	CACGTTTGGGCTTCAAGCTCTGGGGCGGCGGCTTCTTACAGTGGGGGTCATGA	673
Qy	897	CTACTGGCGGCGTACGTCAATCCATCGTCCGCGGCAATCGCGGCTTACCGCGCTTA	956
Db	674	CTACTCGGCGGATATGATCAATCACTCTCTCCGGCATCGCGGCTTACCGCGCTTA	733
Qy	957	CTGGGT 962	
Db	734	CTGGGT 739	

RESULT 10
US-10-437-963-99601
; Sequence 99601, Application US/10437963
; Publication No. US20040123343A1

```

1 GENERAL INFORMATION:
2 APPLICANT: La Rosa, Thomas J.
3 APPLICANT: Kovalic, David K.
4 APPLICANT: Zhou, Yihua
5 APPLICANT: Cao, Yongwei
6 APPLICANT: Wu, Wei
7 APPLICANT: Boukharov, Andrey A.
8 APPLICANT: Barbszuck, Brad
9 APPLICANT: Li, Ping

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: TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
: TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
: FILE REFERENCE: 38-21(53221) B
: CURRENT APPLICATION NUMBER: US/10/437,963
: CURRENT FILING DATE: 2003-05-14
: NUMBER OF SEQ ID NOS: 204966
: SEQ ID NO 99601
: LENGTH: 1764
: TYPE: DNA
: ORGANISM: Oryza sativa
: FEATURE:
: OTHER INFORMATION: Clone ID: PAT_MRT4530_97398C.1
US-10-437-963-99601

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Query Match	10.5%;	Score 387.2;	DB 8;	Length 1764;
Best Local Similarity	77.2%;	Pred. No. 1,1e-65;		
Matches 505; Conservative	0;	Mismatches 128;	Indels 21;	Gaps 2;

QY	309	GTGGGCGACGGTGGTGCCTGGCGGTACAGGGGAAACACTGGCGCTCCGCTGGCGGAACTG	368
Db	37	GTGAGTATGACGGCGCGCGGGCGCTACTCGGCGACGCTACCGG---CGGTCCGGACTG	93
QY	369	GCTGAACAAGGGGACACCGGTGGCAGCTGTGSGCGACGCTGTGGGGCTTGCAAG	428
Db	94	GCTGAACAAGGGGACACCGGTGGCAGCTGACGGCGCGCGCTGTGGGGATCAAGTC	153
QY	429	CGTCCCGGCTTGGTGGTCTGTACCGCGCGGTGTAAAGAAAGTGGGGGTGAATTC	488
Db	154	GATGCCCGGGGTGGTGGTCTGTACCGCGAGCATGTGAAGAAAGTGGGGGTGAATTC	213
QY	489	GGCGTATGAGCGCTTACGCTTCGCGCGCGGTGTGATCTGTGGGTCACTGGGCGCTA	548
Db	214	GGCGTATGAGCGCTTACGCTTACGCGGTGTGCTGTGGTGTGGGTCTGTGGCTT	273
QY	549	CAACATGTCTGTTGGGGGAAAGCTTCCTCCGATTTGGGGGAAAGCGCGCGCTGGA	608
Db	274	CCGATATGGCTTCCGCGACACAGCTGTGCCCTTTGGGGGAAAGCGCGCGCTTAC	333
QY	609	CCAGGGGCTCTGTGGGCGCGCGCGCGCTGCGCGACGAGTCCACTACCGCGCGACG	668
Db	334	CCAGAGCTACTCTGTCCGCGCGCGCGCGAGCTTACCGGACCGCGACCGGCGCATCCGCG	393
QY	669	CAGCGTGAAGACGGCGGCGGTGGAGCGCTGTACCCGATGGCGACGATGTGTACTTCCA	728
Db	394	CACC-----GAGCCCTTCTACCCGGAGGCGACGCTGTGCTTCTTCCA	435
QY	729	GTGGGTGTTCGCGCGCCATCAACCTCATCTCTGTGGCGGCTTCCCTCCGCGCGGATAG	788
Db	436	GTGTGAATGTGCGCGCCATCAAGCTGTCTCTCGCGGCTTCGCTTCGCGCGGATGAA	495
QY	789	CTTCTCGGCGTGAATGATCTTCTGTCCGCGCTGTGGCTCACTTCTCTTCAACGCTGGCGC	848
Db	496	CATCAAGGCGCTGAATGGCTTCAACCCGCTTGGCTCTCTCTCTTCAACGATGGGCGC	555
QY	849	CTTCTCCCTTGGGGCGGCGGCTTCTCTTCACTGGGCGTCATGACTATGCGGCGG	908
Db	556	CTTCAAGCTTGGGGCGGCGGCTTCTCTTCAACGCTGGGCGTCATCGACTCTCGGCGG	615
QY	909	CTTACTATTCACGCTTCCGCGCGCATTCGCGGCTTACCGCGCGTTACTTGGGT	962
Db	616	CTTACTATTCACGCTTCTCTCCGATTCGCGGCTTACCGCGCGTTACTTGGGT	669

RESULT 11
US-10-437-963-81536
; Sequence 81536, Application US/10437963
; Publication No. US20040123343A1

```

; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei

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; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 81536
; LENGTH: 1494
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_81052C.1
; US-10-437-963-81536

Query Match      10.5%; Score 385.4; DB 8; Length 1494;
Best Local Similarity 74.5%; Pred. No. 2.2e-65;
Matches 485; Conservative 0; Mismatches 166; Indels 0; Gaps 0;

QY 312 GGGGACGGTGTGCGCTGCGGACGAGGGAACAGTCGCGCTGCGTGGCGGACTGGCT 371
DB 3 GGGGTGCGCGGACCGCGCGGCGGCGTACATGCGCGCCACCGCGCGTGCAGAGTGGCT 62
QY 372 GAACAAGGGGAGACACGCGTGGAGCTGGTGGCGGACGCTGGTGGGGCTGCAGAGCT 431
DB 63 GAACAAGGGGAGACACGCGTGGAGCTGGTGGCGGACGCTGGTGGGGCTGCAGAGCT 122
QY 432 GCGGCGCTTGTGTGTCTGTACGCGCGCGTGTGAAGAAAGATGGCGGTGAACCTCGG 491
DB 123 GCGTGGCTGTGTGTCTGTACGCGCGCGTGTGAAGAAAGATGGCGGTGAACCTCGG 182
QY 492 GTTCATGTGCGCTGTACGCGCTTCCGCGCGGTGTGTGTGTGTGTGTGTGTGTGTGT 551
DB 183 GTTCATGTGCGCTGTACGCGCTTCCGCGCGGTGTGTGTGTGTGTGTGTGTGTGTGT 242
QY 552 CATGTGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 611
DB 243 CATGTGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 302
QY 612 GGGGCGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 671
DB 303 GGGGCGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 362
QY 672 CGTGAAGAGCGCGCGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 731
DB 363 CGTGAAGAGCGCGCGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 422
QY 732 CGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 791
DB 423 CGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 482
QY 792 CCTGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 851
DB 483 CAAGGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 542
QY 852 CTCCTCTGTGGGCGGCGCTTCTCTTTCACATGAGGCGTGTGTGTGTGTGTGTGT 911
DB 543 CAGCTCTGTGGGCGGCGCTTCTCTTTCACATGAGGCGTGTGTGTGTGTGTGTGT 602
QY 912 CGTGTATCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 962
DB 603 CGTGTATCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 653

RESULT 12
US-10-437-963-86014
; Sequence 86014, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
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; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 86014
; LENGTH: 1494
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_85096C.1
; US-10-437-963-86014

Query Match      10.5%; Score 385.4; DB 8; Length 1494;
Best Local Similarity 74.5%; Pred. No. 2.2e-65;
Matches 485; Conservative 0; Mismatches 166; Indels 0; Gaps 0;

QY 312 GGGGACGGTGTGCGCTGCGGACGAGGGAACAGTCGCGCGTGGCGGACTGGCT 371
DB 3 GGGGTGCGCGGACCGCGCGGCGGCGTACATGCGGACCTGCGCGGTGCAGAGTGGCT 62
QY 372 GAACAAGGGGAGACACGCGTGGAGCTGGTGGCGGACGCTGGTGGGGCTGCAGAGCT 431
DB 63 GAACAAGGGGAGACACGCGTGGAGCTGGTGGCGGACGCTGGTGGGGCTGCAGAGCT 122
QY 432 GCGGCGCTTGTGTGTCTGTACGCGCGCGTGTGAAGAAAGATGGCGGTGAACCTCGG 491
DB 123 GCGTGGCTGTGTGTATCTACGCGCAGATGTGTGAAGAAAGATGGCGGTGAACCTCGG 182
QY 492 GTTCATGTGCGCTGTACGCGCTTCCGCGCGGTGTGTGTGTGTGTGTGTGTGTGTGT 551
DB 183 GTTCATGTGCGCTGTACGCGCTTCCGCGCGGTGTGTGTGTGTGTGTGTGTGTGTGT 242
QY 552 CATGTGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 611
DB 243 CATGTGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 302
QY 612 GGGGCGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 671
DB 303 GGACTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 362
QY 672 CGTGAAGAGCGCGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 731
DB 363 GCTGAGAGCGCGCGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 422
QY 732 CGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 791
DB 423 CGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 482
QY 792 CCTGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 851
DB 483 CAAGGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 542
QY 852 CTCCTCTGTGGGCGGCGCTTCTCTTTCACATGAGGCGTGTGTGTGTGTGTGTGT 911
DB 543 CAGCTCTGTGGGCGGCGCTTCTCTTTCACATGAGGCGTGTGTGTGTGTGTGTGT 602
QY 912 CGTGTATCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 962
DB 603 CGTGTATCAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 653

RESULT 13
US-10-767-701-3848
; Sequence 3848, Application US/10767701
; Publication No. US20040172684A1
```


GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 3848
LENGTH: 623
TYPE: DNA
ORGANISM: Sorghum bicolor
FEATURE:
OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS67017_1
US-10-767-701-3848

Query Match 10.2%; Score 376.4; DB 8; Length 623;
Best Local Similarity 82.8%; Pred. No. 8,3e-64;
Matches 457; Conservative 0; Mismatches 86; Indels 9; Gaps 2;

QY 289 TCAGCGACGAGATGCTGCTGCGGACGATGTCCTGCGCTGACGAGGAGAACAGC 348
DB 78 TCGTCGGCAACTAATGCGCTGCTCGGAGCATGCCACTGACGAG-----ACG 131
QY 349 TCGGCTCGGTGGCGGACCTGCTGAAACAAGGGGAGAACCGCTGGCAGCTGGTGGCGCG 408
DB 132 ACGGGGACCTCCCGGACCTGCTGAAACAAGGGGAGAACCGCTGGCAGCTGACGCGGCG 191
QY 409 ACGCTGTGGGCTGCGAGACGCTGCGGCTGTGTGCTGTGACGCGCGCTGTGTAAG 468
DB 192 ACGCTGTGGGCTGCGAGACCTGCTGCTGCTGTGTGCTGTGACGCGCGCTGTGTAAG 251
QY 469 AAGAAATGGGCGGATGAATCGGCGCTTCAATGCGCTTACGCTTGGCGCGCTGTGATC 528
DB 252 AAGAAATGGGCGGATGAATCGGCGCTTCAATGCGCTTACGCTTGGCGCGCTGTGATC 311
QY 529 TCGTGGGTCACTTGGGCGCTGTAACAATGTGCTTGGGGAGAAAGCTCTCCGATCTGGGG 588
DB 312 TCGTGGGTCACTTGGGCGCTGTAACAATGTGCTTGGGGAGAAAGCTCTCCGATCTGGGG 371
QY 589 AAGGCGCGGCGCGGCTGAGACGAGGCTCTCTGCTGCGCGCGCGCGCTGCGCGAGC 648
DB 312 AAGGCGCGGCGCGGCTGAGACGAGGCTCTCTGCTGCGCGCGCGCGCTGCGCGAGC 431
QY 649 GTCACTACCGCGCGACG---GCAAGCTGTGAGACGCGCGCGGTGGAGCGCTGTACCGG 705
DB 432 GTCACTACTTTCGCCAACGGAAGACATCGAACCGCGCGCGCGGACACTGTATCCG 491
QY 706 AATGGGACGCTGTGTACTTCCAGTGCCTGTTCGCCCATACCTCATCTCTCTGCGC 765
DB 492 AATGGGACGCTGTGTACTTCCAGTGCCTGTTCGCCCATACGCTGTATCTCTGCGC 551
QY 766 GGCCTCCCTCTCGGCGCGATGAGCTTCTGCGCTGTGATCTTCTCCGCTCTGGCTC 825
DB 552 GGCCTCCCTCTCGGCGCGATGAGCTTCTGCGCTGTGATCTTCTCCGCTCTGGCTC 611
QY 826 ACCTTCTCTTAC 837
DB 612 ACCTTCTCTTAC 623

RESULT 14

US-10-425-115-177223
Sequence 177223, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 177223
LENGTH: 1920
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: MRT4577_93216C.1
US-10-425-115-177223

Query Match 10.2%; Score 375.2; DB 9; Length 1920;
Best Local Similarity 77.7%; Pred. No. 2,6e-63;
Matches 474; Conservative 0; Mismatches 118; Indels 18; Gaps 1;

QY 353 CGTCGTGGCGGACCTGCTGAAACAAGGGGAGCAACGCGTGCACTGTGCGCGGACGC 412
DB 328 CGGCGGTCCGAGAGTGGCTTAACAAGGGGAGCAACGCGTGCACTGTGCGCGGACGC 387
QY 413 TGTGGGCTGCAAGAGCTGCGGCTTGTGTGTCTGTATAGCGCGGCGCTGTGAAGA 472
DB 388 TGTGGGCTGCAAGAGCTGCGGCTTGTGTGTCTGTATAGCGCGGCGCTGTGAAGA 447
QY 473 AGTGGCGGATGAATCGGCGCTTCAATGCGCTTACGCTTGGCGCGCTGTGATCTGCT 532
DB 448 AGTGGCGGATGAATCGGCGCTTCAATGCGCTTACGCTTGGCGCGCTGTGATCTGCT 507
QY 533 GGGTCACTGGCGGTAACAATGTGCTGCGGAGAGACCTCTCCGATCTGGGGAGAG 592
DB 508 GGGTCACTGGCGGAGTTCGCAATGCGGCTTGGGAGAGCGCTCTCCGATCTGGGGAGAG 567
QY 593 CGGCGCGGCTGGAACAAGGCGCTTCTGCTGCGCGCGCGCGCGCTGCGCGGAGCGCTC 652
DB 568 CGGCGCGGCTTCTGCAAGGCTTCTGCTGCGCGCGCGCGCGCTGCGCGGAGCGCTC 627
QY 653 ACTTACCGGCGGACGCGGACGCTGAGACGCGGCGGCTGAGACGCGGCTTACCGGAG 712
DB 628 ACGGAGGACGCGCGGACGCGGACGCGGCGGCGGCGGCGGCGGCGGCGGCGGAG 669
QY 713 CGGTGTGTACTTCAAGTGCCTGTTCGCGCGCATACCTCTCACTCTGCGCGGCTCC 772
DB 670 CGGTGTGTGTACTTCAAGTGCCTGTTCGCGCGCATACCTCTGAGTGTCTGCGCGGCTCC 729
QY 773 TCGTGGCGGATGAGCTTCTGCGCTGTGATGATTTGTGCTCCGCTTGGCTCACTTCT 832
DB 720 TCGTGGCGGATGAGCTTCTGCGCTGTGATGATTTGTGCTCCGCTTGGCTCACTTCT 789
QY 833 CCTACACGCTGCGCGCTTCTCTCTGAGGCGGCGGCTTCTCTTCACTGAGGCGCTCA 892
DB 790 CCTACACGCTGCGCGCTTCTCTCTGAGGCGGCGGCTTCTCTTCACTGAGGCGCTCA 849
QY 893 TCGACTACTGCGGCGGCTTCTCTCTGAGGCGGCGGCTTCTCTTCACTGAGGCGCTCA 952
DB 850 TCGACTACTGCGGCGGATGAGCTTCTCTCTGAGGCGGCGGCTTCTCTTCACTGAGGCG 909
QY 953 CTTACTGGGT 962
DB 910 CTTACTGGGT 919

RESULT 15

US-10-437-963-47680
Sequence 47680, Application US/10437963
Publication No. US2004012343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.


```

; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 47680
; LENGTH: 1443
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_50425C.1
; US-10-437-963-47680

Query Match          10.2%; Score 374.2; DB 8; Length 1443;
Best Local Similarity 75.3%; Pred. No. 3,5e-63;
Matches 466; Conservative 0; Mismatches 153; Indels 0; Gaps 0;

QY 344 ACACTGCGGCTGCGTGGCGGACTGGCTGAACAAGGGGGAACAAGCGCTGGCAAGCTGGTG 403
DB 32 AGACCACTCCGTATCGCCAGACTGGCTGAACAAGGGGGAACAAGCGATGGCAATGACAT 91
QY 404 CCGCCGCTGGTGGGGCTGCAAGCGTGCCTGGGCTTGGTGTCTGTACCGGGGGTGG 463
DB 92 CCGCCGACCTCGTGGGCTGCAAGCATGCGAGGCTGGGATCTGTACGGGCAATTG 151
QY 464 TGAAGAAGAAGTGGGGGTGAACCTCGGCGCTTCATGGCGCTTACGCGCTTCCGCCGTG 523
DB 152 TCAAGAAGAAGTGGGCTATCACTCGGCGCTTACGCGCTTGTGCTGTGCTGTCT 211
QY 524 GGAATGCTGGGTCACTGGGCGGTACAAATGTGTTGGGGGAAGCTCTCCGATCT 583
DB 212 GGATCTGTGGGTGTTCTGGGCATACAAATGTGTTGGGCACCGCTCTGCAATCT 271
QY 584 GGGGGAAGCGCGGCGGCTGGACCAAGGCTCTCTCGTGGGCGCGCGCGCGCTGCGCG 643
DB 272 GGGGTAAAGCAGCGGCGGCGGCTGGGCAAGCTCTCTCGTGGGCGAGTCTGAAGTCACTG 331
QY 644 CGACGCTCACTACCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTGTACC 703
DB 332 CTACCGCTATTGGCTTACCAATAGGCTCAAGGCGGCGGCGGCGGCGGCGGCTGTACC 391
QY 704 CGATGGCGAAGGTGTGTATCTTCAGTGGCGTGTTCGCGCGCATCACCTTCATCTGCTG 763
DB 392 CAGTGGCGAAGGTGTGTATCTTCAGTGGCGTGTTCGCGCGCATCACCTTCATCTGCTG 451
QY 764 CCGGCTCCCTCTCGGCGCGCATAGCTTCTCGCTGTGATGATCTTCTGCTCGGCTTGGC 823
DB 452 CAGGCTCACTGCTTGGGCGGCGCATGAACATCAAGGCGGTGATGGCTTGTGCGCTGTGA 511
QY 824 TCACCTTCTCTTACACGATCGTGGCGGCTTCCCTTGGGCGGCGGCGGCTTCTTTCAC 883
DB 512 TCACCTTCTCTTACACGATCGTGGCGGCTTCCCTTGGGCGGCGGCTTCTTTCAC 571
QY 884 GGGGCTCATTCAGCTACTGCGGCGGCTACGCTACATCCAGCTTCGCGCGCATGCGCGCT 943
DB 572 GGGGTGTATAGTACTCTGTGGGTATGTATCATCATCTCTTCTGGCATGCGAGGCC 631
QY 944 TCACCGCGGCTTACTGGGT 962
DB 632 TCACCTGCTGCTACTGGGT 650
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Search completed: July 23, 2006, 21:30:36
Job time : 4207 secs

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QY 121 TATGTTGAATAGAGCAGAGGAGTACATACAGGCTACTAGCCAAACGACGTGAAAT 180
Db 121 TATGTTGAATAGAGCAGAGGAGTACATACAGGCTACTAGCCAAACGACGTGAAAT 180
QY 181 GGTATATCATGAGCCACCTGACACATGCTCTCTATATATAAGCTCCCTTAATAC 240
Db 181 GGTATATCATGAGCCACCTGACACATGCTCTCTATATATAAGCTCCCTTAATAC 240
QY 241 TAGCTAGGATACCAAAAGAAAGCATACCAAGCTTAGTGTGTGTAATCAGCAGAAAG 300
Db 241 TAGCTAGGATACCAAAAGAAAGCATACCAAGCTTAGTGTGTGTAATCAGCAGAAAG 300
QY 301 ATGTGTCGTGGGCGACGGTGGTGGCGCTGGGGTACCAAGGGAAACGTCGGGTCGGT 360
Db 301 ATGTGTCGTGGGCGACGGTGGTGGCGCTGGGGTACCAAGGGAAACGTCGGGTCGGT 360
QY 361 GCGGACTGGCTGAACAAAGGGGACAAACGCTGGCAGCTGGTGGCGGACGCTGGTGGG 420
Db 361 GCGGACTGGCTGAACAAAGGGGACAAACGCTGGCAGCTGGTGGCGGACGCTGGTGGG 420
QY 421 CTGCAGAGCGTGCAGGCTTGGTGGTGTGAACGCGCGGCTGGTGAAGAAAGTGGGCG 480
Db 421 CTGCAGAGCGTGCAGGCTTGGTGGTGTGAACGCGCGGCTGGTGAAGAAAGTGGGCG 480
QY 481 GTGAACCTGGCGGTACATGGGCGCTACGCGCTTCGCGCGGCTGGTGGTGGTGGTGGT 540
Db 481 GTGAACCTGGCGGTACATGGGCGCTACGCGCTTCGCGCGGCTGGTGGTGGTGGTGGT 540
QY 541 TGGGCGTACAAATGTCGTTGGGGGAGAAAGCTCTCCGATCTGGGGGAAAGGCGCGGCG 600
Db 541 TGGGCGTACAAATGTCGTTGGGGGAGAAAGCTCTCCGATCTGGGGGAAAGGCGCGGCG 600
QY 601 GCGCTGGACCAAGGCTCTCTCGTCGGCGCGCGCGCTGGCGGACGCTCCATACCCG 660
Db 601 GCGCTGGACCAAGGCTCTCTCGTCGGCGCGCGCGCTGGCGGACGCTCCATACCCG 660
QY 661 GCGGACGAGGCTGGAGACGCGGCGGAGGAGCGGCTGTACCCGATGGCGAGGAGTGG 720
Db 661 GCGGACGAGGCTGGAGACGCGGCGGAGGAGCGGCTGTACCCGATGGCGAGGAGTGG 720
QY 721 TACTTCCAGTGGGTGTCGCGCGCATCACCTCATCTCGTGGCGCTCCCTCGTGGCG 780
Db 721 TACTTCCAGTGGGTGTCGCGCGCATCACCTCATCTCGTGGCGCTCCCTCGTGGCG 780
QY 781 CGCATGAGCTTCTCGCTGGATGATCTTCGCTCGGCTGTGCTCACTTCTCTCAAC 840
Db 781 CGCATGAGCTTCTCGCTGGATGATCTTCGCTCGGCTGTGCTCACTTCTCTCAAC 840
QY 841 GTGGGCGCTTCCCTCGGCGGCGGCTTCTCTCACTGGGCGGCTCACTGACCTAC 900
Db 841 GTGGGCGCTTCCCTCGGCGGCGGCTTCTCTCACTGGGCGGCTCACTGACCTAC 900
QY 901 TGGCGGCGCTACGTCATCCAGCTTCGCGCGGATGCGCGGCTTCAACGCGCTTAC 960
Db 901 TGGCGGCGCTACGTCATCCAGCTTCGCGCGGATGCGCGGCTTCAACGCGCTTAC 960
QY 961 GTCCGCTACACAGCTCATCTTTTGTCTTATCTTATCTCATCGCAGATTTAAAT 1020
Db 961 GTCCGCTACACAGCTCATCTTTTGTCTTATCTTATCTCATCGCAGATTTAAAT 1020
QY 1021 TTTCAATCAATAATTTAAAGCTAATTTAGAGTTTTTTCATGAGTTATTTTTTATC 1080
Db 1021 TTTCAATCAATAATTTAAAGCTAATTTAGAGTTTTTTCATGAGTTATTTTTTATC 1080
QY 1081 ATTTGTTTTAGTGCCTAAGAACAGTATATATAAGTTTTTATTCACAAATTAATTATCG 1140
Db 1081 ATTTGTTTTAGTGCCTAAGAACAGTATATATAAGTTTTTATTCACAAATTAATTATCG 1140
QY 1141 TTCAAGACTAAGCTAAACATAGTACTCACTTTGGCGCGCGCGCGAGCTGACAGTAG 1200
Db 1141 TTCAAGACTAAGCTAAACATAGTACTCACTTTGGCGCGCGCGCGAGCTGACAGTAG 1200

QY 1201 CTCTGACAAGTGTACATATCATATGTTGGCTGGCAGGTGGGGCCAAAGGCGCAGAGAGAC 1260
Db 1201 CTCTGACAAGTGTACATATCATATGTTGGCTGGCAGGTGGGGCCAAAGGCGCAGAGAGAC 1260
QY 1261 AAGGAGAGGTTCCCGCGCAACATATACGTTTCAACGCTGACGCGGGGCAAGGCTGTGG 1320
Db 1261 AAGGAGAGGTTCCCGCGCAACATATACGTTTCAACGCTGACGCGGGGCAAGGCTGTGG 1320
QY 1321 ATGGGGTGGGAGGTTTCAAGCGGCGGCTCGTACGCGCGCACTCGTGGCCCTATAG 1380
Db 1321 ATGGGGTGGGAGGTTTCAAGCGGCGGCTCGTACGCGCGCACTCGTGGCCCTATAG 1380
QY 1381 GCGGCTCTCAACACCAACATCTGCACCGCATGAGCTCATCTGTCGACATGCTCGAC 1440
Db 1381 GCGGCTCTCAACACCAACATCTGCACCGCATGAGCTCATCTGTCGACATGCTCGAC 1440
QY 1441 GTCATCTTCTTCAAGAGCCCTCGCTCGGCGCGCTGACAGGCGATGATCACCGGCTC 1500
Db 1441 GTCATCTTCTTCAAGAGCCCTCGCTCGGCGCGCTGACAGGCGATGATCACCGGCTC 1500
QY 1501 GTTGGCATCACCCCGCGAGGTACGTAATCATCACTACACGAAACGAAAGCCTT 1560
Db 1501 GTTGGCATCACCCCGCGAGGTACGTAATCATCACTACACGAAACGAAAGCCTT 1560
QY 1561 ATTAATTAAGTATTAAGTAAATACTTAAAGTAAATTAATGATATTTTTTCTTAGA 1620
Db 1561 ATTAATTAAGTATTAAGTAAATACTTAAAGTAAATTAATGATATTTTTTCTTAGA 1620
QY 1621 AAAATTCGCAAAATATACATTTAGTAAATTTTGCATATGTTGTAAAGAAACGAGAG 1680
Db 1621 AAAATTCGCAAAATATACATTTAGTAAATTTTGCATATGTTGTAAAGAAACGAGAG 1680
QY 1681 TTGAAGTTGAAAAAATGAGTACGGAACAAGCCTTATTTATTCATGTTGTGTAGT 1740
Db 1681 TTGAAGTTGAAAAAATGAGTACGGAACAAGCCTTATTTATTCATGTTGTGTAGT 1740
QY 1741 ACTTAATTAATCTTGGAGTGAATGATTAACGCTGATGGCGCGCTGACAGCGCGGA 1800
Db 1741 ACTTAATTAATCTTGGAGTGAATGATTAACGCTGATGGCGCGCTGACAGCGCGGA 1800
QY 1801 TCGATTTCTTAATTAAGTATTAATCCCGGTTTGCATTAATGATCTTCCCGCCGAG 1860
Db 1801 TCGATTTCTTAATTAAGTATTAATCCCGGTTTGCATTAATGATCTTCCCGCCGAG 1860
QY 1861 TTGTTTTACCTTGAATCTAACTGTCTGGGTGGCAACAATACAGAGGTTGGTTACC 1920
Db 1861 TTGTTTTACCTTGAATCTAACTGTCTGGGTGGCAACAATACAGAGGTTGGTTACC 1920
QY 1921 TTGCTGCAAAATATATGCAATTTTCCCGTAGATTAACGCGTTTACATTTTGTGGCA 1980
Db 1921 TTGCTGCAAAATATATGCAATTTTCCCGTAGATTAACGCGTTTACATTTTGTGGCA 1980
QY 1981 CTAATTAAGCAGCAGCAACGCAATGATTCATATCTCTCTCACTCTCTTGTAGTGG 2040
Db 1981 CTAATTAAGCAGCAGCAACGCAATGATTCATATCTCTCTCTCACTCTCTTGTAGTGG 2040
QY 2041 AAGAGTGTAAAGTTTTTATCTCTTGTGCAAGTTGTAGTGAAGTGTAGTGGAGTGGT 2100
Db 2041 AAGAGTGTAAAGTTTTTATCTCTTGTGCAAGTTGTAGTGAAGTGTAGTGGAGTGGT 2100
QY 2101 TTAATTTCCGCTCACTAGTCACTACAGTACCTAATGTGAACAAATATACAGTTCATCGG 2160
Db 2101 TTAATTTCCGCTCACTAGTCACTACAGTACCTAATGTGAACAAATATACAGTTCATCGG 2160
QY 2161 AATCTAGGTTGGTATGATCATATATTCGTCGAAACAGAGAACTTAATTTGTCTTC 2220
Db 2161 AATCTAGGTTGGTATGATCATATATTCGTCGAAACAGAGAACTTAATTTGTCTTC 2220
QY 2221 GTGCTTAATGTCAATGAGAAATACCTATCATAGCTCGTAACTATCTAAAGTCAAGTGG 2280
Db 2221 GTGCTTAATGTCAATGAGAAATACCTATCATAGCTCGTAACTATCTAAAGTCAAGTGG 2280
QY 2281 TCTGAACGTGCCAATTTGTTTTTCTGAGTTTTTCTGTACGCAAGCAGCCAAAGAAAG 2340

DB 2281 TGTGAACCTGCCAATTTGTTTTTTTCTGAGTTTTTTTGTAGCGACGACGCAAGAAAAG 2340
QY 2341 CACACTGAAAAATGAAAGTAATTTTTCACGCTCCCATTCGCTGGTGACTTCGTTCA 2400
DB 2341 CACACTGAAAAATGAAAGTAATTTTTCACGCTCCCATTCGCTGGTGACTTCGTTCA 2400
QY 2401 AAGTCTATTTAGCGCGCGAGATGAGCTACAGTACTCCATAGCAATTTGTCATGACATCA 2460
DB 2401 AAGTCTATTTAGCGCGCGAGATGAGCTACAGTACTCCATAGCAATTTGTCATGACATCA 2460
QY 2461 GGCAGCTGTACGTCTATCGCAAGAGATCCGTCTTATTTATGACACATGACACACC 2520
DB 2461 GGCAGCTGTACGTCTATCGCAAGAGATCCGTCTTATTTATGACACATGACACACC 2520
QY 2521 TACACCCCTTATCATTTATTTGTTTTTGAATTTGTCGTAATAACAGATTTCAATAGA 2580
DB 2521 TACACCCCTTATCATTTATTTGTTTTTGAATTTGTCGTAATAACAGATTTCAATAGA 2580
QY 2581 GCATTAACATTAATGATTTTCTTTTCCGTACACACAGCAATCTCAATAAATTTATCTC 2640
DB 2581 GCATTAACATTAATGATTTTCTTTTCCGTACACACAGCAATCTCAATAAATTTATCTC 2640
QY 2641 TTTTGTATCAAAACATAGTAATCTTTGTACTGAATTAATCTCTGCTCCATAAATAAT 2700
DB 2641 TTTTGTATCAAAACATAGTAATCTTTGTACTGAATTAATCTCTGCTCCATAAATAAT 2700
QY 2701 CATTTTAAATTTCTATGTCACAACTTTGATCATCCGTTTATTTAAAAAATTTAAT 2760
DB 2701 CATTTTAAATTTCTATGTCACAACTTTGATCATCCGTTTATTTAAAAAATTTAAT 2760
QY 2761 TTTTATTAATAATGTCATACATTAAGTATTTATTTATTTATTTATTTAATAAATAAG 2820
DB 2761 TTTTATTAATAATGTCATACATTAAGTATTTATTTATTTATTTATTTAATAAATAAG 2820
QY 2821 AATATTAATTAATAATAATAATAATAAGAGAGAAATCAAAACGGTATGAGATTGATTG 2880
DB 2821 AATATTAATTAATAATAATAATAATAAGAGAGAAATCAAAACGGTATGAGATTGATTG 2880
QY 2881 CAGGGGTGTGACGAGGGTGGCGCGCTGTGTATGAGGGGTGCTCGCGGAGCATCCGT 2940
DB 2881 CAGGGGTGTGACGAGGGTGGCGCGCTGTGTATGAGGGGTGCTCGCGGAGCATCCGT 2940
QY 2941 GGTACACCATGATGATCTTCACAAAGGCTCCAAATCTCTGACGCGGTGACGACACC 3000
DB 2941 GGTACACCATGATGATCTTCACAAAGGCTCCAAATCTCTGACGCGGTGACGACACC 3000
QY 3001 TCGGCGCTTTCCACACCGACGCGGTGCGCGCTCTCGCGCGGCTCTCAACGCGCTCT 3060
DB 3001 TCGGCGCTTTCCACACCGACGCGGTGCGCGCTCTCGCGCGGCTCTCTCAACGCGCTCT 3060
QY 3061 TCGGCGAGCCCACTCTGTGCACTCTCTCTCCCGTCCCGGACTCCCGGGGGGCTTCT 3120
DB 3061 TCGGCGAGCCCACTCTGTGCACTCTCTCTCCCGTCCCGGACTCCCGGGGGGCTTCT 3120
QY 3121 ACGGCGGCGCGCGCGCGCGCACTTCGCGCAAGAGATCGCGCGGCGCTTCTGTGCTG 3180
DB 3121 ACGGCGGCGCGCGCGCGCGCACTTCGCGCAAGAGATCGCGCGGCGCTTCTGTGCTG 3180
QY 3181 CCGTGAACGTGCTGCTCACTCTCTCTCACTGCTCTCGCAATCACTCTCTCTCTCTCC 3240
DB 3181 CCGTGAACGTGCTGCTCACTCTCTCTCACTGCTCTCGCAATCACTCTCTCTCTCTCC 3240
QY 3241 GCATGCCGACGACAGCTGAGGTGCGACGACGCGCTCCACGCGGAGAGAGGCTTACG 3300
DB 3241 GCATGCCGACGACAGCTGAGGTGCGACGACGCGCTCCACGCGGAGAGAGGCTTACG 3300
QY 3301 CGCTCTGGGGGCGACGCGGAGATGATGACGTCACAAAGCGGCTCGACGCGCGCTT 3360
DB 3301 CGCTCTGGGGGCGACGCGGAGATGATGACGTCACAAAGCGGCTCGACGCGCGCTT 3360
QY 3361 CCCCCCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3420
DB 3361 CCCCCCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3420

DB 3361 CCCCCCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3420
QY 3421 AAGAAATTTATACACAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3480
DB 3421 AAGAAATTTATACACAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3480
QY 3481 AATCTATGTTCAAGTTTACGTGATTTTAAACAGCGCGCTGAGTATGAGCATTTGCACT 3540
DB 3481 AATCTATGTTCAAGTTTACGTGATTTTAAACAGCGCGCTGAGTATGAGCATTTGCACT 3540
QY 3541 TTGACAGATTCAAGGAGTCCGCTCTGATTTTGTAGTTTGTAAAAATGATACGTAG 3600
DB 3541 TTGACAGATTCAAGGAGTCCGCTCTGATTTTGTAGTTTGTAAAAATGATACGTAG 3600
QY 3601 TTTTGTATCTTACTGATCTGATCTGATGATGATGATGATGATGATGATGATGATGAT 3660
DB 3601 TTTTGTATCTTACTGATCTGATCTGATGATGATGATGATGATGATGATGATGATGAT 3660
QY 3661 CTCATATTTTCCAAA 3677
DB 3661 CTCATATTTTCCAAA 3677

RESULT 2

US-10-449-902-24969
; Sequence 24969, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agricultural Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A02051-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; PRIOR FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 24969
; LENGTH: 1790
; TYPE: DNA
; ORGANISM: Oryza sativa
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AK100411
; DATABASE ENTRY DATE: 2002-08-28
US-10-449-902-24969

Query Match 20.3%; Score 746.4; DB 6; Length 1790;
Best Local Similarity 97.7%; Pred. No. 1.9e-133;
Matches 780; Conservative 0; Mismatches 11; Indels 7; Gaps 2;

QY 2879 TGCAGGGGTGTGTCAGGGGTGGCGCGCTGTGATGAGGGGTGCTGCGCGGACGATGCC 2938
DB 996 TGCAGGGGTGTGTCAGGGGTGGCGCGCTGTGATGAGGGGTGCTGCGCGGACGATGCC 1055
QY 2939 GTGGTACACATGATGATCTCTCCACAAAGGCTCCAAAGATCTGACAGCGGTGACGACAC 2998
DB 1056 GTGGTACACATGATGATCTCTCCACAAAGGCTCCAAAGATCTGACAGCGGTGACGACAC 1115
QY 1116 CCGCGGCGCTTCTCAACCAAGCGGTGCGCGGCTCTCGCGGCGCTCTCAACCGGCTT 1175
DB 3059 CTTGCGCGACCCACCTCTGCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3118
QY 1176 CTTGCGCGACCCACCTCTGCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1235
DB 3119 CTAAGCGGCG 3178

Db 1236 CTACGGCGGCGCGGCGGCGCCAGTTCCGAGCAGATCCGCGGTGCTTCTGTCGT 1295
Qy 3179 CGCCTGGAAACGTCGTGTACCTCCCTCATCTGCTCCGATCAACCTCTGTCCTCGT 3238
Db 1236 CGCCTGGAAACGTCGTGTACCTCCCTCATCTGCTCCGATCAACCTCTGTCCTCGT 1355
Qy 3239 CGCAGTCCCGACGACAAAGCTCGAGTCGCGACGACGCGCTCCACGCGGAGGAGGCTTA 3298
Db 1356 CGCAGTCCCGACGACAAAGCTCGAGTCGCGACGACGCGCTCCACGCGGAGGAGGCTTA 1415
Qy 3239 CGCGCTCTGGGGCGACGCGGAGATGTACGACGCTCAACGACGCGCTCCGACGCGCGCT 3358
Db 1416 CGCGCTCTGGGGCGACGCGGAGATGTACGACGCTCAACGACGCGCTCCGACGCGCGCT 1475
Qy 3359 TCGCCCGCTGCTGTGTATGATCATCTTAATTGATGTGCTGTCTGATGTAACCC 3418
Db 1476 TCGCGCCGCTGTGTATGATCATCTTAATTGATGTGCTGTGTAACCC 1531
Qy 3419 TCAAGAAATTCATACACAGAAATTAATACGATGCTGCTCTGCTTAATTATG 3478
Db 1532 TCAAGAAATTCATACACAGAAATTAATACGATGCTGCTCTGCTTAATTATG 1591
Qy 3479 AAAATCTATGTTCAAGTTTACGTGTATTAAACGCGCGCTGTGAG---TTAGGCAAT 3535
Db 1592 AAAATCTATGTTCAAGTTTACGTGTATTAAACGCGCGCTGTGAGTTTAAAGTATT 1651
Qy 3536 GCACCTTGGAAATTCAGGGGAGTCCGCTCTGTATTTTGTAGTTGTAATAATGTA 3595
Db 1652 GCACCTTGGAAATTCAGGGGAGTCCGCTCTGTATTTTGTAGTTGTAATAATGTA 1711
Qy 3596 CGTAGTTTGTATTCCTTACGTGATCTGAATGAACAAAGTAAATTAATTATTTGTTAA 3655
Db 1712 CGTAGTTTGTATTCCTTACGTGATCTGAATGAACAAAGTAAATTAATTATTTGTTAA 1771
Qy 3656 TTAAGCTCCATATTTTCC 3673
Db 1772 TTAAGCTCCATATTTTCC 1789

RESULT 3
US-10-449-902-18930
; Sequence 18930, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agricultural Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 18930
; LENGTH: 1441
; TYPE: DNA
; ORGANISM: *Oryza sativa*
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AK069311
; DATABASE ENTRY DATE: 2001-12-06
US-10-449-902-18930

Query Match 20.0%; Score 733.6; DB 6; Length 1441;
Best Local Similarity 98.0%; Pred. No. 4,9e-131;
Matches 766; Conservative 0; Mismatches 9; Indels 7; Gaps 2;
Qy 2879 TGCAGGGGTGTGCAAGGGGTGGCGCGCTGTGTATGGGGGTGCTCCCGGAGCATCCC 2938
|||||

Db 664 TGCAGGGGTGTGCAAGGGGTGGCGCGCTGTGTATGGGGGTGCTCCCGGAGCATCCC 723
Qy 2939 GTGTGACACCAATGATGATCTTCAACAGCGCTCAAGATTCCTGACAGCGGTCGACAC 2998
Db 724 GTGTGACACCAATGATGATCTTCAACAGCGCTCAAGATTCCTGACAGCGGTCGACAC 783
Qy 2999 CCTCGGCTCTTTCACACACCAAGCGGTGCGGCGCTCCTCGGCGGCTCTCTCAACGCGCT 3058
Db 784 CCTCGGCTCTTTCACACACCAAGCGGTGCGGCGCTCCTCGGCGGCTCTCTCAACGCGCT 843
Qy 3059 CTTGCGGAGCCACCTCTTCAACCTTCTTCTCCCGTCCGACCTCCGAGGCGCTT 3118
Db 844 CTTGCGGAGCCACCTCTTCAACCTTCTTCTCCCGTCCGACCTCCGAGGCGCTT 903
Qy 3119 CTACGGCGGCG 3178
Db 904 CTACGGCGGCG 963
Qy 3179 CGCCTGGAAACGTCGTGTACCTCCCTCATCTGCTCCGATCAACCTCTGTCCTCGCT 3238
Db 964 CGCCTGGAAACGTCGTGTACCTCCCTCATCTGCTCCGATCAACCTCTGTCCTCGCT 1023
Qy 3239 CGCAGTCCCGACGACAACTCTGAGTGGCGACGACGCGCTCCACGCGGAGGCGCTTA 3298
Db 1024 CGCAGTCCCGACGACAACTCTGAGTGGCGACGACGCGCTCCACGCGGAGGCGCTTA 1083
Qy 3299 CGCGCTCTGGGGCGACGCGCGGAGTGTACAGCTCAACAGAGCGCTCCGACGCGCGCT 3358
Db 1084 CGCGCTCTGGGGCGACGCGCGGAGTGTACAGCTCAACAGAGCGCTCCGACGCGCGCT 1143
Qy 3359 TCGCCCGCTGCTGTATGATCATCTTAATTGATGCTGTCACTGATGTAACCC 3418
Db 1144 TCGCGCGCTGTGTATGATCATCTTAATTGATGCTGTCACTGATGTAACCC 1199
Qy 3419 TCAAGAAATTCATACACAGAAATTAATACGATGCTGCTGCTTAATTATG 3478
Db 1200 TCAAGAAATTCATACACAGAAATTAATACGATGCTGCTGCTTAATTATG 1259
Qy 3479 AAAATCTATGTTCAAGTTTACGTGTATTAAACGCGCGGTGAG---TTAGGCAAT 3535
Db 1260 AAAATCTATGTTCAAGTTTACGTGTATTAAACGCGCGGTGAGTTTAAAGTATT 1319
Qy 3536 GCACCTTGCAGATTCAGGGGAGTCCGCTCTGTATTTTGTAGTTGTAATAATGTA 3595
Db 1320 GCACCTTGCAGATTCAGGGGAGTCCGCTCTGTATTTTGTAGTTGTAATAATGTA 1379
Qy 3596 CGTAGTTTGTATTCCTTACGTGATCTGAATGAACAAAGTAAATTAATTATTTGTTAA 3655
Db 1380 CGTAGTTTGTATTCCTTACGTGATCTGAATGAACAAAGTAAATTAATTATTTGTTAA 1439
Qy 3656 TT 3657
Db 1440 TT 1441

RESULT 4
US-10-713-648A-46
; Sequence 46, Application US/10713648A
; Publication No. US20060107344A1
; GENERAL INFORMATION:
; APPLICANT: POSCO
; APPLICANT: POSTECH
; APPLICANT: An, Gynheung
; APPLICANT: Ryu, Choong-Hwan
; APPLICANT: Han, Jong-Jin
; APPLICANT: Kang, Hong-Gyu
; APPLICANT: An, Kyungsok
; TITLE OF INVENTION: ORGAN PREFERENTIAL GENES IDENTIFIED BY T-DNA INSERTIONAL
; FILE REFERENCE: 2001-0-04USA
; CURRENT APPLICATION NUMBER: US/10/713,648A
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/427,166

Oy		824	TCACCTTCTCTAACACCGGTGGGCGCTTCTCCCTCTGGAGGGGGGGGCTTCCCTTCCACT	883
Db		831	TCACCTTCTCTAACACCGCTTCCCGCTTCTTGCTCTGGAGGGGGGGGCTTCTTCCACT	890
Oy		884	GGGGCGCATCAGCACTATGCGCGGCTACGTATCAAGCTCTCCGCCGCATCGCGGCT	943
Db		891	GGGGGTCATCGACTACCTCCGGCGGCTACGTATCAACTCATCTCTCTCGGAATCGCCGGCC	950
Oy		944	TCACCGCGCTTACTGGGT	962
Db		951	TCACCGCGCTTACTGGGT	969
 RESULT 7 US-10-449-902-11675 ; Sequence 11675, Application US/10449902 ; Publication No. US20060123505A1 ; GENERAL INFORMATION: ; APPLICANT: National Institute of Agrobiological Sciences. ; APPLICANT: Bio-oriented Technology Research Advancement Institution. ; APPLICANT: The Institute of Physical and Chemical Research. ; APPLICANT: Foundation for Advancement of International Science. ; FILE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF ; TITLE REFERENCE: MOA-AO205Y1-US ; CURRENT APPLICATION NUMBER: US/10/449, 902 ; PRIOR FILING DATE: 2003-05-29 ; PRIOR APPLICATION NUMBER: JP 2002-203269 ; PRIOR FILING DATE: 2002-05-30 ; PRIOR APPLICATION NUMBER: JP 2002-383870 ; PRIOR FILING DATE: 2002-12-11 ; NUMBER OF SEQ ID NOS: 56791 ; SOFTWARE: Patentln Ver. 2.1 ; SEQ ID NO 11675 ; LENGTH: 1140 ; TYPE: DNA ; ORGANISM: Oryza sativa ; PUBLICATION INFORMATION: ; DATABASE ACCESSION NUMBER: AKI09023 ; DATABASE ENTRY DATE: 2002-08-28 US-10-449-902-11675				
 Query Match 10.6%; Score 389.2; DB 6; Length 1140; Best Local Similarity 74.0%; Pred. No. 4.3e-65; Matches 493; Conservative 0; Mismatches 173; Indels 0; Gaps 0				
Oy		237	GAAATGTCGTCGTCGCGGAGCGTGTGTCCTCGCGCGTAACAAGGGGAACAGCTCGCGCTC	356
Db		56	GAAAGAAGTAGTAGTGAGTGCGCCACCAGCCGCGCGGAGCGGTACATGCGCGCCACCGGC	115
Oy		357	GATGCGGACTATGCTGTAACAAGAGGGGGAACAAGCGCTGAGAGCTGATGCGCGGACAGCTGTG	416
Db		116	GATGCGGAGTAGCTGTAACAACCGGGGGAACAAGCGATGAGGAGCTCGCGCGGCAAGTTGCT	175
Oy		417	GGGGCTGAGAGCGTGGCGGGGCTTGTGTGCTGTACAGCGCGGCGTGTGTAAGAAGAGTG	476
Db		176	CGGGCTCAGTGCATGCTCTGGGCTGTGTGCTGTACAGCACATGTAAGAAGAGAGTG	235
Oy		477	GGCGGTGAATCGGGGTTCATGAGCGCTCTACGCCCTTCCCGCGCGTGTGATATGCTGGGT	536
Db		236	GGCGGTCAACTCGGCTTCATGAGCGCTGTACCGGTACGGTCAAGCTTCATGTGTGGGT	295
Oy		537	CACCTGGCGGTAAACATGTCGTTGGGGGAGAAAGTCTCCCGATCTGGGAGAAAGCGCG	596
Db		236	GCTGTGCGGCTTCCGCAATGCGCTTGGCGAACCGGCTGTGCTCCGTTCTGGGGGAAAGCGCG	355
Oy		597	GCCGCGCTGGAACAGGGGCTTCTCTGTGCGGCGCGCGCCGCGCTGCCGCGAGGATCCACTA	656
Db		356	CGCGCGCTGACAGGAGGGGATTCTGTGTGCGCGCGCGTGTGCTCCGGCCACAGGCGCACTA	415
Oy		657	CCGCGCGCAAGCGCAACGTCGAGAGCGCGCGCGGTGAGCGCGCTGTAACCGATGAGCGAGGT	716
Db		416	CGGAGAGACCGCGGCTTGAGATGCGCGCGGACCAAGCGGTTTCAACCGAGGCGTTCAT	475

QY 717 GGTGTTCTTCCATGCTGTGTCGGCCGATCAACCTTCATCTGTGCGCGCTCCCT 776
DB 476 GGTGCTTTCATGTTGAGTTCGCGCCATCAAGCTGTGTCTGTGCGCGCTCCCT 535
QY 777 CGGCGCCATGAGCTTCTGCTGCGATGATCTTGTGCGCTGTGCTCACTTCTCTTA 836
DB 536 CGGAGAGATTAATCAAGCCGTGATGAGCTTCACTCCGCTGTGCTCTCTCTTA 595
QY 837 CACCGTGGCGCTTCTCTCTGCGCGCGCTTCTCTTTCACCTGAGGCGTATCGA 896
DB 596 CACCGTGGCGCTTCTCTGAGCTTGTGCGCGCGCTTCTCTTACAGTGGGCGTCAATCGA 655
QY 897 CTAATCGCGCGCTGATGATATCAAGCTTCGCGCGCGATCGCGGCTTCAACCGCGCTTA 956
DB 656 CTAATCGCGCGATGATGATCACTCTCTCTCGCGATCGCGGCTTCAACCGCGCTTA 715
QY 957 CTGGGT 962
DB 716 CTGGGT 721

RESULT 8

US-10-449-902-14739
; Sequence 14739, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; PRIOR FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14739
; LENGTH: 1957
; TYPE: DNA
; ORGANISM: Oryza sativa
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AK065288
; DATABASE ENTRY DATE: 2001-12-06
US-10-449-902-14739

Query Match 10.6%; Score 388; DB 6; Length 1957;
Best Local Similarity 78.9%; Pred. No. 9,4e-65;
Matches 481; Conservative 0; Mismatches 111; Indels 18; Gaps 1;

QY 353 CGTCGATGGGGAAGTGTGTAACAAGGAGGACAACCGTGGCGAGCTGTGTCGGCGCGC 412
DB 287 CGCGGTGTCGCACTGCTGAACAAGGAGGACAACCGTGGCGAGCTGTGTCGACGCGC 346
QY 413 TGTGTGGGAGTGCAGAGCGTGCCTGGTGTGTGTGCTGTACGCGCGGTGTGAAGAGA 472
DB 347 TGTGTGGGAGTGCAGTGCATGTCGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 406
QY 473 AGTGGCGGTGAACCTGGCGCTTCAATGCGCTTACGCGCTTTCGCGCGGTGTGTGTGT 532
DB 407 AGTGGCGGTGAACCTGGCGCTTCAATGCGCTTACGCGCTTTCGCGCGGTGTGTGTGT 466
QY 533 GGTGTCACTGGGAGTGAACAATGTCTTGGGAGGAGCTTCCTCCGATTTGGGAGGAG 592
DB 467 GGTGTCTGTGTGCTTTCGATGCGCTTTCGAGCAACGCTGTGCGCTTTCGAGGAGG 526
QY 593 CGGCGCGGCGCTGACCAAGGCGCTTCTGTGCGCGCGCGCGCTGCGCGAGCGTCC 652
DB 527 CGGCGCGGCGCTGACCAAGGCGTACTCTGTGCGCGCGCGCGCGCGCGCGCGCGCG 586

QY 653 ACTACCGCGCGACCGGACGCTGAGAGACGCGCGGCTGAGCGCGCTATCCGATGAGCA 712
DB 587 ACGGCGCCATCCCGCGAC-----GAGCCCTTCTACCGGAGGCCA 628
QY 713 CGATGTGATCTTCCAGTGCAGTGTTCGCGCGATCAACCTCATCTGTGCGCGGCTCC 772
DB 629 CGGTGTGTCTTCCAGTGTGAGTTCGCGCGATCAACGCTGTGCTCTGTGCGCGCTCCG 688
QY 773 TCTGTGCGCGGATGAGCTTCTGCGCGCTGATGATCTGTGCTCCGCTGTGCTCACTTCT 832
DB 689 TCTGTGCGCGGATGAGCAATCAAGCGCTGTGATGCGCTTACCGCGCTGTCTCTCT 748
QY 833 CTAACCGGTGGCGCGCTTCTGCTGTGAGGCGCGGCTTCTCTTCACTGAGGAGTGA 892
DB 749 CTAACCGGTGGCGCGCTTCTGAGCTTCTGTGAGGCGCGGCTTCTCTACGCTGAGGAGTGA 808
QY 893 TCGACTACTCGCGCGCTATGATCAAGTCTCGCGCGATCGCGGCTTCAACCGCG 952
DB 809 TCGACTACTCGCGCGCTATGATCAAGTCTCTCTCGCGATCGCGGCTTCAACCGCG 868
QY 953 CTTACTGGGT 962
DB 869 CTTACTGGGT 878

RESULT 9

US-10-449-902-6821
; Sequence 6821, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; PRIOR FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6821
; LENGTH: 1687
; TYPE: DNA
; ORGANISM: Oryza sativa
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AK063959
; DATABASE ENTRY DATE: 2001-12-06
US-10-449-902-6821

Query Match 10.5%; Score 385.4; DB 6; Length 1687;
Best Local Similarity 74.5%; Pred. No. 2.8e-64;
Matches 485; Conservative 0; Mismatches 166; Indels 0; Gaps 0;

QY 312 GCGCAAGTGTGTCGCTGCGCTGACCAAGGAGAACAGTGCAGCTGTGTCGGCGAGTGGCT 371
DB 4 GCGGTGCGCGCGGACCG 63
QY 372 GAAACAAGGAGACACCGCTGAGCTGTGTGCGCGAGACGCTGTGTGGGCTGTGAGAGCT 431
DB 64 GAAACAAGGAGACACCGCTGAGCTGTGTGCGCGAGACGCTGTGTGGGCTGTGAGAGCT 123
QY 432 GCGCGCTTGT 491
DB 124 GCGT 183
QY 492 GTTCATGAGCGCTTACGCTTGTGCGCGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 551
DB 184 GTTCATGAGCGCTTACGCTTGTGCGCGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 243

QY 552 CATGTCGTTGCGGAGAAAGCTCTCCGATCTGGGGGAAAGCGCGGCGCGGTGAGACA 611
DB 244 CATGCGCTTCGCGGAGACCGGCTCTCCGTTCTGGGGCAAAGCCGAGCCGCGCTGACGA 303
QY 612 GGGCCCTCTCTGTCGCGCGCGCGCTGCGCGAGCGGTCACTACCGCGCGAGCGGAG 671
DB 304 GGAATCTTCGTTGGTCAACGCGCGGTTGTCCCGCGAGCGGCACTACCGAGAGAGGAGC 363
QY 672 CGTGAAGAGCGCGCGGTTGAGACCGCTGTACCCGATGCGAGCGTGTACTTCCAGTG 731
DB 364 GCTTCAGAGCGCGCGCAACCGACCGCTTCTACCGGAGGCGCGCTGTGTCTGTGAGTT 423
QY 732 CGTGTTCGCGCGCATACCGCTCATCGTGTGCGCGGCTCTCTCTCGCGCGGATGAGCT 791
DB 424 CGAGTTTCGCGGCACTACCGCTGTGTCTGCTCGCGGCTCTCTCTCGCGCGGATGAGCT 483
QY 792 CCGTCCGCTGAGTATCTTCTGTCGCGCTCTGAGCTTCTCTACACCGCGCGGCTT 851
DB 484 CAAGGCGTGGATGAGGCTTACCGCGCTGCGCTCTCTCTCTACACCGCGCGGCTT 543
QY 852 CTCCTCTGCGGCGCGGCTTCTCTCTGCACTGGGCGCTCATGACTACTGCGGCGCTA 911
DB 544 CAGCCTCTGGGCGCGCGGCTTCTCTCTACAGTGGGCGCTCATGACTACTGCGGCGGATA 603
QY 912 CGTCATCCACGCTCTCGCGCGGATGCGCGGCTTCAACCGCGCTTACTGAGT 962
DB 604 CGTCATCCACGCTCTCTCTCGCGGCTGCGCGGCTTCAACCGCGCTTACTGAGT 654

RESULT 10

US-10-449-902-26664
; Sequence 26664, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A02051-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26664
; LENGTH: 1719
; TYPE: DNA
; ORGANISM: Oryza sativa
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AK102106
; DATABASE ENTRY DATE: 2002-08-28
US-10-449-902-26664

Query Match 10.5%; Score 385.4; DB 6; Length 1719;
Best Local Similarity 74.5%; Pred. No. 2.8e-64;
Matches 485; Conservative 0; Mismatches 166; Indels 0; Gaps 0;

QY 312 GCGGACGCTGCTGCGCTGCGGATGCAAGGGAACAGTGGGGTTCGCTGCGGACTGAGCT 371
DB 66 GCGGTGCGCGCGGACCGGCGGCGGCTGATGCGGAGCTGCGGCGGCTGCGGCGGCT 125
QY 372 GAACAAGGAGGACAACGCTGCGAGCTGCTGCGCGAGCGCTGTGTGGGCTGCGAGAGCT 431
DB 126 GAACAAGGAGGACAACGCTGCGAGCTGCTGCGCGAGCGGAGCGGCTGTGTGTGAGT 185
QY 432 GCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 491
DB 186 GCGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 245

QY 492 GTTCATGCGGCTCTACGCTTTCGCGCGGCTGTGATCTGCGGCTTCACTGAGGAGTCAA 551
DB 246 CTTATGAGCGCTTGAAGCTTACCGCTTACCGCTTATCGTGTGGTGTCTCTGCGCTTCCG 305
QY 552 CATGTCGTTGCGGAGAAAGCTCTTCCGATCTGGGAGAAAGCGCGCGGCTTGGAGCA 611
DB 306 CATGCGCTTCGCGGAGACCGGCTGTCTCCGTTCTGGGCGCAAAGCCGAGCGCGGCTGACGA 365
QY 612 GGGCTCTCTGTCGCGCGCGCGGCTGCGCGAGCGGTCACTACCGCGCGAGCGGAG 671
DB 366 GGAATCTTCGTTGGTCAACGCGCGGTTTCCCGGCAACCGGCACTACCGGAGAGGAGC 425
QY 672 CGTGAAGAGCGCGCGGTTGAGACCGCTGTACCCGATGCGAGCGTGTACTTCCAGTG 731
DB 426 GCTGAAGAGCGCGCGGCAACCGGCTTCTACCGGAGGCGGCGCTGTGTGTGAGTT 485
QY 732 CGTGTTCGCGCGCATACCGCTCATCTGCTGCGCGGCTCTCTCTCGCGCGGATGAGCT 791
DB 486 CGAGTTTCGCGGCACTACCGCTGTGTGTCTGCTGCGCGGCTCTCTCTCGCGCGGATGAGCT 545
QY 792 CCGTCCGCTGAGTATCTTCTGTCGCGCTCTGAGCTACCTTCTCTACACCGCGCGGCTT 851
DB 546 CAAGGCGTGGATGAGGCTTACCGCGCTGTGCTCTCTTCTCTACACCGCGCGGCTT 605
QY 852 CTCCTCTGCGGCGCGGCTTCTCTCTGCACTGGGCGCTCATGACTACTGCGGCGGCTA 911
DB 606 CAGCCTCTGGGCGCGCGGCTTCTCTCTACAGTGGGCGCTCATGACTACTGCGGCGGATA 665
QY 912 CGTCATCCACGCTCTCGCGCGGATGCGCGGCTTCAACCGCGCTTACTGAGT 962
DB 666 CGTCATCCACGCTCTCTCTCGCGGCTGCGCGGCTTCAACCGCGCTTACTGAGT 716

RESULT 11

US-10-449-902-11363
; Sequence 11363, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A02051-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11363
; LENGTH: 1870
; TYPE: DNA
; ORGANISM: Oryza sativa
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AK108711
; DATABASE ENTRY DATE: 2002-08-28
US-10-449-902-11363

Query Match 10.1%; Score 372.6; DB 6; Length 1870;
Best Local Similarity 75.1%; Pred. No. 8.2e-62;
Matches 465; Conservative 0; Mismatches 154; Indels 0; Gaps 0;

QY 344 ACACGTCGCGCTGCTGCGGATGCTGTAACAAGGAGGACAACGCTGCGAGCTGCTGG 403
DB 417 AGACACCTCCGTCATCGCGAGCTGCTGTAACAAGGAGGACAACGCTGCGAGATGAT 476
QY 404 CGGCAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 463
DB 477 CGGCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 536

QY 464 TGAAGAAGATGGGGGCTGAATCGGCGTTCAATGAGCGCTTACAGGCTTGGCCCGGTGT 523
DB 537 TCTAAGAAGATGGGGGCTGAATCGGCGTTCAATGAGCGCTTACAGGCTTGGCCCGGTGT 596
QY 524 GATCTGCTGGGTCACTGGGCGCTTACAAATGCTGTTGGGAGAAAGCTCTCCGATCT 583
DB 597 GATCTGCTGGGTGCTGGGCGCTTACAAATGCTGTTGGGAGAAAGCTCTCCGATCT 656
QY 584 GGGGGAAGCGCGCGCGCGCTGAGACAGGCGCTCTCGTGGCGCGCGCGCTGCGG 643
DB 657 GGGGTAAGGACAGCGCGCGCGCTGAGACAGGCGCTCTCGTGGCGCGCGCTGCGG 716
QY 644 CGACGCTCACTACCGCGCGCGCTGAGACAGGCGCGCGCGCTGAGACCGCTGAC 703
DB 717 CTACCGCTATTCGCTACCAATGAGGTGAGTGGGCGCGCGCTGAGACCGCTGAC 776
QY 704 CGATGCGACGAGGTGCTGCTTCACTGAGTGGCGCGCGCTGAGACCGCTGAC 763
DB 777 CAGTGGCACAGATGCTGCTTCACTGAGTGGCGCGCGCTGAGACCGCTGAC 836
QY 764 CGGCTCTCTCTCGCGCGCGCTGAGTGGCGCGCGCTGAGTGGCGCGCTGAG 823
DB 837 CAGGCTCACTGCTGGCGCGCTGAGTGGCGCGCGCTGAGTGGCGCGCTGAG 896
QY 824 TACCTCTCTCTCACTGAGTGGCGCGCTTCTCTCTGCGCGCGCGCTTCTCTCACT 883
DB 897 TACCTCTCTCTCACTGAGTGGCGCGCTTCTCTCTGCGCGCGCGCTTCTCTCACT 956
QY 884 GGGGCGCTCACTGAGTGGCGCGCTTCTCTCTGCGCGCGCGCTTCTCTCACT 943
DB 957 GGGGCTCACTGAGTGGCGCGCTTCTCTCTGCGCGCGCGCTTCTCTCACT 1016
QY 944 TCACCGCGCGCTTACTGGGT 962
DB 1017 TCACCTGCTGCTACTGGGT 1035

RESULT 12
US-10-713-648A-12
Sequence 12, Application US/10713648A
Publication No. US20060107344A1
GENERAL INFORMATION:
APPLICANT: POSCO
APPLICANT: POSTECH
APPLICANT: An, Gynheung
APPLICANT: Ryu, Choong-Hwan
APPLICANT: Han, Jong-Jin
APPLICANT: Kang, Hong-Gyu
TITLE OF INVENTION: ORGAN PREFERENTIAL GENES IDENTIFIED BY T-DNA INSERTIONAL
FILE REFERENCE: 20010-04USA
CURRENT APPLICATION NUMBER: US/10/713,648A
PRIOR FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: 60/427,166
NUMBER OF SEQ ID NOS: 83
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12
LENGTH: 401
TYPE: DNA
ORGANISM: Oryza sativa
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)...(96)
OTHER INFORMATION: segment of the T-DNA insert in line 1C-109-35
US-10-713-648A-12

Query Match 8.5%; Score 312; DB 6; Length 401;
Best Local Similarity 97.0%; Pred. No. 1,7e-50;
Matches 318; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY 2307 TGAATTTTCTTGTACGCAAGCAGCCAGAAAGACACATGAAATGAAATGATATT 2366

DB 74 TGTGATTATTAAGTGTCTAAGCAGCCAGAAAAGACACATGAAATGAAATGATATT 133
QY 2367 TTACAGCTCCCAATTCCTGCTGAGTCTGTTCAAAAGTCTATTACCGCGCAGATGGA 2426
DB 134 TTACAGCTCCCAATTCCTGCTGAGTCTGTTCAAAAGTCTATTACCGCGCAGATGGA 193
QY 2427 CTACAGTACTCCATGACATTTGTGATGATCATGAGCAGTGTCTATGTCGAAGA 2486
DB 194 CTACAGTACTCCATGACATTTGTGATGATCATGAGCAGTGTCTATGTCGAAGA 253
QY 2487 TCCGTGCTCTTATTTATGACACATGACACATGACACATGACACATGACACATG 2546
DB 254 TCCGTGCTCTTATTTATGACACATGACACATGACACATGACACATGACACATG 313
QY 2547 TTGATTTGTGCTATTAATGACATGATTTCAATGAGATTAATGATTTTCTTTTC 2606
DB 314 TTGATTTGTGCTATTAATGACATGATTTCAATGAGATTAATGATTTTCTTTTC 373
QY 2607 GTTAAACACAGCAATCTCAATTAATAT 2634
DB 374 GTTAAACACAGCAATCTCAATTAATAT 401

RESULT 13
US-11-216-545-4910
Sequence 4910, Application US/11216545
Publication No. US20060135758A1
GENERAL INFORMATION:
APPLICANT: MONSANTO Technology, LLC
APPLICANT: McIaird, Paul L
APPLICANT: Tao, Nengbing
APPLICANT: Wu, Kunsheng
TITLE OF INVENTION: Single Nucleotide Polymorphic Markers and Methods of Genotyping
FILE REFERENCE: 38-21 (53659)B
CURRENT APPLICATION NUMBER: US/11/216,545
PRIOR FILING DATE: 2005-08-31
PRIOR APPLICATION NUMBER: US 60/606,062
PRIOR FILING DATE: 2004-08-31
NUMBER OF SEQ ID NOS: 8783
SOFTWARE: PatentIn version 3.2
SEQ ID NO 4910
LENGTH: 1551
TYPE: DNA
ORGANISM: Glycine max
US-11-216-545-4910

Query Match 7.9%; Score 289.6; DB 8; Length 1551;
Best Local Similarity 67.0%; Pred. No. 6.1e-46;
Matches 409; Conservative 0; Mismatches 201; Indels 0; Gaps 0;
QY 353 CGTGGTGGCGGAGTGGTGAACAAAGGGGACAAAGCGTGGCAGCTGTGGCGGACCG 412
DB 305 CGGCGGACCCGAAATGGCTGAACAAGGTGACAAAGCGTGAACGAGCGACGCC 364
QY 413 TGTGTGGGCTGACAGACGCTGCGGCTGTGTGTCTGTACGCGCGCGTGTGAAGA 472
DB 365 TGTGTGGGCTTCAAAACATGCGCGGCTGTGTGTCTGTACGCGCGCGTGTGAAGAAA 424
QY 473 AGTGGCGGTGAACCTGGGCTTATGCGCTGACGCTTGGCGCGGTGTGATCTGCT 522
DB 425 AATGGGAGTGAACCTAGCTTATGAGCTTCTTACGCTTGGCGCGGTCTTAATATGTT 484
QY 533 GGTGTACCTGGGCGTGAACATGCTGTTGGGAGAGCTCTCCGATCTGGGGAAGG 592
DB 485 GGTGTGCTGTGTGTACCGAATGCTTTGAGAGAAACCTTTCCCTTCTGGGGAAGG 544
QY 593 CGGCGCGGCGCTGACAGGCGCTCTGTGTGGCGCGCGCGCGCGCGCGCGCGCTCC 652
DB 545 GTGCTCCAGACATGAGCCAGAAAGTCTTCCAGAAAAGACATGATGATTTGAATCC 604
QY 653 ACTACCGCGCGCAGCGGAGGTGAGACGCGCGGTGAGAGCGGCTGTACCGGATGGCGA 712

Db 605 ACCACTTTGATATATGSCATGTTGTAATCACTTCGAGGAAACCTTTTACCTATGAGCCT 664
Qy 713 CGGTGCTGATCTTCCAGTCCGCTGTTGCGCCCATACCTCTATCTCTGTCGGCTCCC 772
Db 665 CGCTGTGTATTTCCAAATTCACCTTTTGCTGCTATTACTCTATTTGTTGGCTGGCTCG 724
Qy 773 TCCTGCGCGCATGAGCTTCTCGCTGATGATCTTGGTCCGCTCTGAGCTCACTTCT 832
Db 725 TCCTTGGCCGAATGACATCAAGGCTTGGATGAGCTTTTGCTCTTTGGTGTGATCTTTT 784
Qy 833 CCTACACGCTCGCGCTTCTCTCTCTGAGGCGCGCTTCTCTTCCATGAGGCGCTCA 892
Db 785 CCTACACAGTCCGGGCTTTAGCTTTTGAGCTTTGAGGCTTTTCTCTACCAATGGGCGTTA 844
Qy 893 TCGACTACTGCGCGCGCTCACTCACTCACTCTCGCGCGCATCGCGGCTTACCGCGC 952
Db 845 TTGACTATTTCTGGCGGCTATGTCATCCACCTTTCTTGGAAATCGCTGGTTTAACTGTG 904
Qy 953 CTTACTGGGT 962
Db 905 CTTACTGGGT 914

RESULT 14

US-10-953-349-17238

; Sequence 17238, Application US/10953349

; Publication NO. US20060107345A1

; GENERAL INFORMATION:

; APPLICANT: ALEXANDROV, Nikolai et al.

; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES

; FILE REFERENCE: 2750-1579PUS2

; CURRENT APPLICATION NUMBER: US/10/953,349

; CURRENT FILING DATE: 2004-09-30

; NUMBER OF SEQ ID NOS: 40252

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 17238

; LENGTH: 805

; TYPE: DNA

; ORGANISM: Glycine max

US-10-953-349-17238

Query Match 7.6%; Score 278; DB 6; Length 805;

Best Local Similarity 66.6%; Pred. No. 7.5e-44;

Matches 398; Conservative 0; Mismatches 200; Indels 0; Gaps 0;

Qy 365 ACTGCTGAACAAGGGGACAAAGCGCTGACCTGCTGCGCGCGAGCTGTGGGCTGC 424
Db 86 ACTGCTAAACAAGGGGACAAAGCATGAGCACTGACAGCAGCACTCTCTAGTCTCC 145
Qy 425 AGAGGCTGCGGGCTTGTGTGTCTCTAGCGCGCGCTGTGAAGAAAGTGGCGCTGA 484
Db 146 AAAGATGCGCGGCTGTGTGTCTCTCTAGCGAGCATGTGTGAAGAAAGTGGCGCTGA 205
Qy 485 ACTCGCGCTTCAATGCGCTCTAGCTTCTGCGCGCGCTGTGAATCTGCTGGTCACTTGG 544
Db 206 ACTCTGCACTTCAATGCGCTCTAGCTTCTGCGCGCGCTGTGAATCTGCTGGTCACTTGG 265
Qy 545 CATAACAATGCTGT 604
Db 266 GTCAACGAATGCGCTGT 325
Qy 605 TGGACAGAGGCTCTCTCTGCGCGCGCGCGCGCGCGCGCGAGCTGCACTACCGCGCG 664
Db 326 TAGGCGAAGATTTTAAACACACCGCGCGCAAAAGTCCCGAAGACGACCTATTAACA 385
Qy 665 ACGGAGCGTGTGAAGACGCGCGGTGAGCGCTGTACCGGATGCGGAGCGTGTGTACT 724
Db 386 ATGTATGCTGTGAAGACGCGCGCTGTGAGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 445
Qy 725 TCCAGT 784

Db 446 TTCAATTCACGTTTGGCGCTATACGCTTATCTTGTGGCGGATCGGTGAGAGAA 505
Qy 765 TGAGCTTCTCGCCCTGAGTATCTTGTGTCGCGCTGTGCTACCTTCTCTACACGTG 844
Db 506 TGAACATCAAGGCTGTGAGT 565
Qy 845 GCGCTTCTCTCTCTGCGGCGCGCGCTTCTCTTCTCACTGTGGGCGCTCACTACG 904
Db 566 GGGCTTATAGCTTTTGGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 625
Qy 905 GCGCTACGTCATCCACGCTTCTCGCGCGGATGCGCGCTTCAACCGCGCTTACTGGT 962
Db 626 GTGATATGTTATTCATCTTCTCTGTGAATGCTGTGCTTCACTGCTCTTACTGGGT 683

RESULT 15

US-10-953-349-10297

; Sequence 10297, Application US/10953349

; Publication NO. US20060107345A1

; GENERAL INFORMATION:

; APPLICANT: ALEXANDROV, Nikolai et al.

; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES

; FILE REFERENCE: 2750-1579PUS2

; CURRENT APPLICATION NUMBER: US/10/953,349

; CURRENT FILING DATE: 2004-09-30

; NUMBER OF SEQ ID NOS: 40252

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 10297

; LENGTH: 1648

; TYPE: DNA

; ORGANISM: Arabidopsis thaliana

US-10-953-349-10297

Query Match 5.8%; Score 214.8; DB 6; Length 1648;

Best Local Similarity 61.7%; Pred. No. 1.3e-31;

Matches 379; Conservative 0; Mismatches 202; Indels 33; Gaps 1;

Qy 349 TCGGCGTGGTGGCGGAGCTGCTGAACAAGGGGACAAAGCGCTGAGCTGGTGGCGCG 408
Db 107 TTGCGGAGGTTCTGTAATGCTCAACAAGGAGACAAAGCGCTGAGCTCAAGCGAGCG 166
Qy 409 ACGCTGTGGGCTGCAAGCGTGGCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 468
Db 167 ACTGT 226
Qy 469 AAGAGTGGCGGCTGAATCTGCGCTTCAATGCGCTCTTACGCTTGTGCGCGCTGTGATC 528
Db 227 AAGAAATGGGCTGTGAATTCAGCTTTTATGTGCTTTTACGCTTTTGTGCGCGCTTGTTC 286
Qy 529 TGCTGGTCACTGGGCGGTAACAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 588
Db 287 TGT 346
Qy 589 AAGGCGCGCGCGCTGAGCAGGCGCTCTCTGTGCGCGCGCGCGCGCTGTGCGCGAGC 648
Db 347 AAAGT 399
Qy 649 GTTCACTACCGCGCGGAGCGGCTGTGAGACGCGCGGTGTGAGACCGCTGTACCGGATG 708
Db 400 -----AAATGTATATGTGGCGCGCGCTGTATTTTCCGATG 433
Qy 709 GCGAGGTGTGTATCTTCCAGT 768
Db 434 GCGAGGTGTGTATTTTCAATTCATTTGCGGCGGATTAAGACATCTGTGTGCGGGA 493
Qy 769 TCCCTCTCGCGCGATGAGCTTCTCTGCTGTGATGATCTTGTCTGCTGTGCTGTGCTAC 828
Db 494 TCTGT 553
Qy 829 TTCTCTTACACGCTGTGCGCGCTTCTCTCTGTGCGCGCGCGCTTCTCTTCACTGTGGC 888
Db 554 TTTAGCTACAGTGTGAGCTTATATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 613

QY 889 GTGATGACTACTGCGGCGCTAGTCATCCACGCTCCGCGGCAATCGCGGCTTCACC 948
Db 614 GTTATTGATTATTCGCGCGGTATGTTATTCATCTCTCCGCGGTGCGGTTTCGTC 673
QY 949 GCGGTTACTGGGT 962
Db 674 GCTGTTACTGGGT 687

Search completed: July 24, 2006, 02:05:07
Job time : 474 secs

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OM protein - protein search, using sw model

Run on: July 22, 2006, 03:24:06 ; Search time 196 Seconds
(without alignments)
1117.381 Million cell updates/sec

Title: US-10-713-648A-63

Perfect score: 2534
Sequence: 1 MSSSATVVPVPLAYQNTSASV.....GEMVDYTKRGSDAAVAVPVV 479

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003s:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2534	100.0	479	8	ADP09672 Rice ammo
2	2216	87.5	470	8	Aao26538 Wheat hlg
3	2216	87.5	470	10	Aef16014 Trifolium
4	1891.5	74.6	509	8	ADY09035 plant ful
5	1860.5	73.4	486	6	Aao26537 Soybean h
6	1860.5	73.4	486	10	Aef16012 Glycine m
7	1715.5	67.7	497	6	Aao26536 Rice high
8	1715.5	67.7	497	10	Aef16010 Oryza sat
9	1682.5	66.4	475	5	ABR92034 Herbicida
10	1357	53.6	325	7	ABM87942 Rice abio
11	1357	53.6	325	7	ABM90348 Rice abio
12	1352	53.4	440	7	ABM89810 Rice abio
13	717.5	28.3	455	7	ABO74999 Pseudomon
14	693.5	27.4	476	7	ABM87991 Rice abio
15	652	25.7	413	5	ABM84938 Lactococc
16	652	25.7	428	6	ABM70704 Photocarb
17	646	25.5	223	8	ADX89780 plant ful
18	641	25.3	439	7	ABO64443 Klebsiell
19	640.5	25.3	488	6	ABP77916 N. gonorr
20	639	25.2	433	7	ADP05820 Bacterial
21	634.5	25.0	470	6	ADA34110 Actinoba
22	619.5	24.4	470	7	ABM87867 Rice abio
23	589.5	23.3	401	5	ABR49278 Listeria

24	589	23.2	428	6	ADA89710 Staphyloc
25	589	23.2	428	6	ABM70882 Staphyloc
26	586.5	23.1	431	5	ABP65520 Bifidobac
27	583.5	23.0	191	8	ADX72255 Plant ful
28	582	23.0	437	5	ABP39062 Staphyloc
29	582	23.0	437	8	ADP07046 Staphyloc
30	565	22.3	438	4	AAG93227 C glutam
31	532	21.0	463	9	ABM96125 M. xanthu
32	532	20.6	479	8	ADR86206 Apep9111
33	508	20.0	480	4	ADP98897 C. albica
34	476	18.8	452	4	AAE76708 Corynebac
35	476	18.8	452	4	AAE93214 C glutam
36	474.5	18.7	492	8	ADR87095 Yeast Str
37	422.5	16.7	924	4	ABG26085 Novel hum
38	342	13.5	651	4	ABR62422 Drosophil
39	338.5	13.4	501	2	AAE74676 Arabidops
40	338.5	13.4	501	3	AAE40620 Arabidops
41	338.5	13.4	510	3	AAE36233 Arabidops
42	335	13.2	361	7	ADH88022 Enterococ
43	335	13.2	514	8	ADN74427 Thale cre
44	322	12.7	431	7	ADM25447 Hyperther
45	320	12.6	446	3	AAG40621 Arabidops

ALIGNMENTS

RESULT 1	ADP09672	ADP09672 standard; protein; 479 AA.
ID	XX	ADP09672;
AC	XX	ADP09672;
DT	XX	26-AUG-2004 (first entry)
XX	XX	
DE	XX	Rice ammonium transporter protein without the T-DNA insert SeqID 63.
KW	XX	rice; ammonium transporter; GUS; insertional mutagenesis;
KW	XX	beta-glucuronidase; biotic stress resistance; pesticide; herbicide;
XX	XX	plant; hygromycin phosphotransferase; HGH; T-DNA; transfer-DNA.
OS	XX	Oryza sativa.
PN	XX	WO2004046357-A1.
PD	XX	03-JUN-2004.
PR	XX	14-NOV-2003; 2003WO-KR002461.
PF	XX	15-NOV-2002; 2002US-0427166P.
XX	XX	(POSC-) POSCO.
PA	XX	(POST-) POSTECH FOUNO.
XX	XX	An G, Ryu C, Han J, Kang H, An K;
XX	XX	WPI; 2004-449751/42.
DR	XX	N-PSDB; ADP09638, ADP09655.
XX	XX	New organ preferential nucleic acids and polypeptides, useful in
PT	XX	producing rice plants with desired characteristics and which are
PT	XX	resistant to herbicide, plant pathogen, fungi, bacteria, virus, insect,
PT	XX	nematode, and stress.
XX	XX	Claim 15, SEQ ID NO 63; 296pp; English.
XX	XX	This invention relates to a novel method of identifying nucleic acid
CC	XX	molecules, or fragments thereof, that are expressed in an organ
CC	XX	preferential manner in rice. Specifically, it refers to producing rice
CC	XX	cell lines that carry tagged genes modified by T-DNA/GUS based
CC	XX	insertional mutagenesis, where the GUS portion of the insert is the
CC	XX	promoterless beta-glucuronidase reporter gene that can only be expressed
CC	XX	when it is inserted into an active gene. The present invention describes

CC generating transformed rice lines containing transfer-DNA (T-DNA)
CC insertions that also carry a gene encoding the selectable marker
CC hygromycin phosphotransferase (Hph). Accordingly, this method can be used
CC to produce rice plants with desirable characteristics including increased
CC grain yield and nutritional content, resistance to biotic stresses,
CC pesticides, herbicides or insects, altered morphology or improved
CC characteristics referring to shape, taste or cooking quality of the
CC grain. This polypeptide sequence represents a rice protein encoded by a
CC gene that will be T-DNA/GUS tagged for expression analyses, given in an
CC exemplification of the invention.

SQ Sequence 479 AA;

Query Match 100.0%; Score 2534; DB 8; Length 479;

Best Local Similarity 100.0%; Pred. No. 8.8e-235;

Matches 479; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 MSSATVPLAAYQNTSASVADMLKGNAMQLVAATLVGLQSVPLVLYGGVKKKMA 60
DB 1 MSSATVPLAAYQNTSASVADMLKGNAMQLVAATLVGLQSVPLVLYGGVKKKMA 60
QY 61 VNSAFMALYAFAAVVICWVTAAVYNSFGEKLLPIWGKAPALDQGLVGRALPATVHYR 120
DB 61 VNSAFMALYAFAAVVICWVTAAVYNSFGEKLLPIWGKAPALDQGLVGRALPATVHYR 120
QY 121 ADGSETAVERLYPMATVYFQCVFAATLLVAGSLIGRMSFLAMMIFVPLMTFSYV 180
DB 121 ADGSETAVERLYPMATVYFQCVFAATLLVAGSLIGRMSFLAMMIFVPLMTFSYV 180
QY 181 VGAFSLMGSGFLFHMGVLDYCGGYVHVSAIGAGFTAAVWGPRAQKREPPNNILFT 240
DB 181 VGAFSLMGSGFLFHMGVLDYCGGYVHVSAIGAGFTAAVWGPRAQKREPPNNILFT 240
QY 241 LTGAGLLMWGMAGFNGGGPYAANSVASAVLNTNICTAMSLVWTCLDVIFPKKSVGA 300
DB 241 LTGAGLLMWGMAGFNGGGPYAANSVASAVLNTNICTAMSLVWTCLDVIFPKKSVGA 300
QY 301 VOGMTITGLVCTIPRAGVVOGMAALVMGVLAGSIPWYTMMLHKRSKILQVDDTLGVFHT 360
DB 301 VOGMTITGLVCTIPRAGVVOGMAALVMGVLAGSIPWYTMMLHKRSKILQVDDTLGVFHT 360
QY 361 HGVAGLLGLLTGLFAEPTLCNLFLPVADSRGAFYGGAGAGQFGKQIAGLFFVAMNVV 420
DB 361 HGVAGLLGLLTGLFAEPTLCNLFLPVADSRGAFYGGAGAGQFGKQIAGLFFVAMNVV 420
QY 421 TSLICLAINLLVPLAMPDDKLEVGDDAVHGEBAVYALMGDEMYDVTKHGSDAAVAPVV 479
DB 421 TSLICLAINLLVPLAMPDDKLEVGDDAVHGEBAVYALMGDEMYDVTKHGSDAAVAPVV 479
```

RESULT 2

AAO26538 standard; protein; 470 AA.

AAO26538;

18-FEB-2003 (first entry)

Wheat high affinity ammonium transporter protein #2.

Herbicide; ammonium transporter protein; herbicide; transgenic plant;

wheat.

Triticum aestivum.

US2002142390-A1.

03-OCT-2002.

28-DEC-2001; 2001US-00033109.

28-AUG-1998; 98US-0098248P.

27-AUG-1999; 99US-00384625.

XX (AILE/) ALLEN S M.
PA (RAFA/) RAFALSKI J A.
XX Allen SM, Rafalski JA;
XX MPI; 2003-102520/09.
DR N-PSDB; AAL53990.

PT Novel ammonium transporter polypeptide useful for identifying enzymatic
PT inhibitors, which is homologous to corn, soybean, wheat or rice ammonium
PT transporter polypeptides.

Claim 14; Page 24-25; 27pp; English.

CC The invention relates to a novel ammonium transporter protein comprising
CC 90% homology based on the Clustal method compared to: a corn ammonium
CC transporter polypeptide of 183 or 63 amino acids; a soybean ammonium
CC transporter polypeptide of 500 or 486 amino acids; a wheat ammonium
CC transporter polypeptide of 494 or 470 amino acids; and a rice ammonium
CC transporter 497 amino acids fully defined in the specification. The
CC isolated polynucleotide is useful for selecting an isolated
CC polynucleotide that affects the level of expression of the ammonium
CC transporter polypeptide in a plant cell. The ammonium transporter protein
CC is useful for preparing antibodies which are useful for detecting the
CC transporter protein in situ in cells or in vitro in cell extracts, and as
CC targets to facilitate design and/or identify inhibitors of the enzymes
CC that are useful as herbicides. The isolated polynucleotide is also useful
CC for creating transgenic plants in which the polynucleotide is present at
CC higher or lower levels than normal, and for designing and producing
CC primer pairs which are useful in amplification or primer extension
CC reactions. This sequence represents the wheat high affinity ammonium
CC transporter protein of the invention

SQ Sequence 470 AA;

Query Match 87.5%; Score 2216; DB 6; Length 470;

Best Local Similarity 86.0%; Pred. No. 3.6e-204;

Matches 404; Conservative 30; Mismatches 34; Indels 2; Gaps 1;

```
QY 8 VPLAYQNTSASVADMLKGNAMQLVAATLVGLQSVPLVLYGGVKKKMAVNSAFMA 67
DB 3 VPVAYQNTSAAVADMLKGNAMQLTASTLVGLMSYGMVLYGGVKKKMAVASAFMA 62
QY 68 LYAFAAVVICWVTAAVYNSFGEKLLPIWGKAPALDQGLVGRALPATVHYRADGSYET 127
DB 63 LYAFAAVVICWVTAAVYNSFGEKLLPIWGKAPALDQGLVGRALPATVHYRADGSYET 122
QY 128 AAVEPLYPMATVYFQCVFAATLLVAGSLIGRMSFLAMMIFVPLMTFSYTVGAFSLW 187
DB 123 AMVEPYPMATVYFQCVFAATLLVAGSLIGRMSFLAMMIFVPLMTFSYTVGAFSVW 182
QY 188 GGGFLFHMGVLDYCGGYVHVSAIGAGFTAAVWGPRAQKREPPNNILFTLTGAGLL 247
DB 183 GGGFLFHMGVLDYCGGYVHVSAIGAGFTAAVWGPRAQKREPPNNILFTLTGAGLL 242
QY 248 WMGAGFNGGGPYAANSVASAVLNTNICTAMSLVWTCLDVIFPKKSVGAQOGMTTG 307
DB 243 WMGAGFNGGGPYAANSVASAVLNTNICTAMSLVWTCLDVIFPKKSVGAQOAVTTG 302
QY 308 LVCITPRAGVVOGMAALVMGVLAGSIPWYTMMLHKRSKILQVDDTLGVHTHGVAGLL 367
DB 303 LVCITPRAGVVOGMAALVMGVLAGSIPWYTMMLHKRSKILQVDDTLGVHTHGVAGLL 362
QY 368 GGLLTGLFAEPTLCNLFLPVADSRGAFYGGAGAGQFGKQIAGLFFVAMNVVTSLICLA 427
DB 363 GGLLTGLFAEPTLCNLFLPVADSRGAFYGGAGAGQFGKQIAGLFFVAMNVVTSIICV 422
QY 428 INLLVPLAMPDDKLEVGDDAVHGEBAVYALMGDEMYDVTKHGSDAAVAPV 477
DB 423 IRLVPLKMSSEKLAIGDDAVHGEBAVYALMGDEMYDVTKHG--AAVVPV 470
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Query Match	87.5%; Score 2216; DB 10; Length 470;
Best Local Similarity	86.0%; Pred. No. 3,6e-204;
Matches	404; Conservative 30; Mismatches 34; Indels 2; Gaps 1.
XX AEF16014	standard; protein; 470 AA.
XX ID AEF16014	standard; protein; 470 AA.
XX AC AEF16014;	
XX DT 09-MAR-2006	(first entry)
XX DE Trt1c1um aestivum ammonium transporter protein SegID14.	
XX KW ammonium transfer; transgenic plant; nitrogen; cellular transport.	
XX OS Trt1c1um aestivum.	
XX PN US2006010512-A1.	
XX PD 12-JAN-2006.	
XX PF 15-DEC-2004; 2004US-00012668.	
XX PR 28-DEC-2001; 2001US-00033109.	
XX PA (ALLE/) ALLEN S M.	
XX PA (RAFA/) RAFALSKI J A.	
XX PI Allen SM, Rafalski JA;	
XX XX WPI; 2006-088761/09.	
XX DR N-PSDB; AEF16013.	
XX XX	
PT New isolated polynucleotide encoding a polypeptide having ammonium	
PT transfer activity, useful for producing transgenic plants with increased	
PT nitrogen content.	
XX XX	
XX Example 4; SEQ ID NO 14; 29pp; English.	
CC This invention relates to a novel isolated polynucleotide encoding a	
CC polypeptide having ammonium transfer activity. The polynucleotides are	
CC useful for producing transgenic plants with increased nitrogen content.	
CC The present sequence is an ammonium transporter protein which is encoded	
CC by a nucleotide sequence homologous to the sequence of the invention.	
XX XX	
XX Sequence 470 AA;	
Query Match	87.5%; Score 2216; DB 10; Length 470;
Best Local Similarity	86.0%; Pred. No. 3,6e-204;
Matches	404; Conservative 30; Mismatches 34; Indels 2; Gaps 1.
QY 8 VPLAYQGTSAASVADWLNKGNAMQVLAATLVGLQSVGLVYLKGVVKKKAAVNSAFMA	67
DB 3 VPVAYQGTSAAVADVDMLNKGNAMQVLAATLVGLQSVGLVYLKGVVKKKAAVNSAFMA	62
QY 68 LYAPAAVVICWWTAAVYNSFGFKLPIWGKAPALDOGLVGRALPATVHYRADGSYET	127
DB 63 LYAPAAVVICWWTAAVYNSFGFKLPIWGKAPALDOGLVGRALPATVHYRADGSYET	122
QY 128 AAVEBLYEMATVYVQCVFAAITLLIVAGSLGRMSFLAMMIFVBLMTFSYTVGAFSLM	187
DB 123 AMVEBLYEMATVYVQCVFAAITLLIVAGSLGRMSFLAMMIFVBLMTFSYTVGAFSLM	182
QY 188 GGGFLFHWGVIDYCGGYIYIHVSAGIAGFTAAVWGPRAOKRERPPNNILFTLTGAGLL	247
DB 183 GGGFLFHWGVIDYCGGYIYIHVSAGIAGFTAAVWGPRAOKRERPPNNILFTLTGAGLL	242
QY 248 WMGAGFGGGSYYAANVSAAVLAATNTCTAASLIVWCLDVIFFPKKSVGAVOGMITG	307
DB 243 WMGAGFGGGSYYAANVSAAVLAATNTCTAASLIVWCLDVIFFPKKSVGAVOGMITG	302
QY 308 LVCTIPAGAGVVOGMAALVMGVLAGSI PMYTMILHKRSKILQVDDTLGVFHTHVGAGLL	367
DB 303 LVCTIPAGAGVVOGMAALVMGVLAGSI PMYTMILHKRSKILQVDDTLGVFHTHVGAGLL	362
QY 368 GGLLTGLFAEPTLNCULFLPVADSRGAFYGGAGGAOFGKOIAGGLVVAAMVVVTSICLA	427

D6 363 GGATGTGTAEPNLCNLEPVTNSRGAFFYGNGAGQOLGRKQIALGVIGMNVVYTSIIICVV 4422

Oy 428 INILIVLRHPDDKLKVGDPAVHGEEAYALMDGGEMVDYTKHGSDAAPAVP 477
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
D6 423 IRLVPLRMSEETLAIGDPVAHGEEAYALMDGGEMVDYTKHG--AAVPV 470

RESULT 4
ID ADY09035 standard; protein, 509 AA.
AC ADY09035;
XX ADY09035;
DT 21-APR-2005 (first entry)
DE Plant full length insert polypeptide seqid 64850.
KW plant protectant; plant growth regulant; gene therapy; plant;
KW recombinant DNA construct; physical array; plant breeding marker;
KM cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
KM extreme osmotic condition; pathogen tolerance; pest tolerance;
KM growth rate; cell cycle pathway; disease resistance;
KW galactomannan production; lignin production; plant growth regulator;
KM yield; plant growth; plant development; seed oil; protein yield;
protein content.
XX unidentified.
OS Unidentified.
PN US2004034888-A1.
PD 19-FEB-2004.
PF 28-APR-2003; 2003US-00425114.
PR 06-MAY-1999; 99US-00304517.
PR 05-NOV-2001; 2001US-00985678.

(LIU/J) LIU J,
(ZHOU/) ZHOU Y,
(KOVA/) KOVALIC D K,
(SCRE/) SCREEN S E,
(TABAS/) TABASKA J E,
(CAO/Y) CAO Y.

Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
PI WPI; 2004-160133/17.
DR New recombinant DNA construct, useful for improving plant tolerance to
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
PT pests, for conferring increased resistance to plant disease, or for
PT improving yield.
XX Claim 1, SEQ ID NO 64850; 15pp; English.

The invention describes a recombinant DNA construct comprising a
polynucleotide consisting of a sequence encoding an amino acid sequence
available in electronic form from the US patent office at
<ftp://seqdata.uspto.gov/sequence.html?DocID:2004034888>. The polynucleotide
of the invention are also useful in physical arrays of molecules and as
plant breeding markers. The recombinant DNA construct is useful for
improving plant tolerance to cold, heat, drought, herbicides, extreme
osmotic conditions, pathogens or pests, for manipulating growth rate in
plant cells by modification of the cell cycle pathway, for conferring
increased resistance to plant disease, for producing galactomannan,
lignin or plant growth regulators, for increasing the rate of homologous
recombination in plants, for improving yield by modification of
photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
or by providing improved plant growth and development under at least one
stress condition or for modifying seed oil or protein yield and/or
content. This is the amino acid sequence of a plant full length insert
polypeptide that can be used in the recombinant DNA construct of the

CC invention.
XX Sequence 509 AA;

Query Match 74.6%; Score 1891.5; DB 8; Length 509;
Best Local Similarity 72.9%; Pred. No. 76-173;
Matches 341; Conservative 57; Mismatches 61; Indels 9; Gaps 4;

11 AYGQTSASVADMLKNDAMQVLAATLVGLQSPGLVYL YGCVYKKKVAVNSAFMALYA 70
DB AYO--SSSSPMLNKGDMQMTSHVLGLQSPGLVYL YGCVYKKKVAVNSAFMALYA 95
QY 71 FAAVVICWVTAAVYNNSPFGEKLPYNGKARPAIDQGLVGRALPAT-VHYRADGSVETAA 129
DB 96 FAAVVICWVTAAVYNNSPFGEKLPYNGKARPAIDQGLVGRALPAT-VHYRADGSVETAA 154
QY 130 VEPLYPMATVYFQCVPAATITLIVAGSLGKMSFLAMMI FVPLMLTTSYTYGAFLMG 189
DB 155 LHPFYPAATMVYFQCVPAATITLIVAGSLGKMSFLAMMI FVPLMLTTSYTYGAFLMG 214
QY 190 GFLPHMGVIDYCGGVYVHVSAGIAGFTAAVYVGPRAOKRERPPNNILFTLTGAGLLM 249
DB 215 GFLPHMGVIDYCGGVYVHVSAGIAGFTAAVYVGPRAOKRERPPNNILFTLTGAGLLM 274
QY 250 GWAGFNGGPPYANASVAMVAVLNTNICTAMSLIWTCLDVIFFKKPSVAVQGMITGLV 309
DB 275 GWAGFNGGPPYANASVAMVAVLNTNICTAMSLIWTCLDVIFFKKPSVAVQGMITGLV 334
QY 310 CITPAAGVYQGMALVYMGVLAAGSIPTWYTMILHKSKILQVDDTLGVHHTGAVAGLLG 369
DB 335 CITPAAGVYQGMALVYMGVLAAGSIPTWYTMILHKSKILQVDDTLGVHHTGAVAGLLG 394
QY 370 LLTGLFAEPTLCNLFPLVADSRGAFYGGAGAGOFQKQIAGLFEVYANVNTSLICLAI 429
DB 395 ATTGFAEPTLCNLFPLVADSRGAFYGGAGAGOFQKQIAGLFEVYANVNTSLICLAI 454
QY 430 LLVPLRMPDDKLEVGDDAVHGEBAAYALMGDGEWYDT----KHGSDA 472
DB 455 LLVPLRMPDDKLEVGDDAVHGEBAAYALMGDGEWYDT----KHGSDA 502

RESULT 5
AA026537 standard; protein; 486 AA.

AA026537;

18-FEB-2003 (first entry).

Soybean high affinity ammonium transporter protein #2.

Herbicide; ammonium transporter protein; herbicide; transgenic plant;
soybean.

Glycine max.

US2002142390-A1.

03-OCT-2002.

28-DEC-2001; 2001US-00033109.

28-AUG-1998; 98US-0098248P.

27-AUG-1999; 99US-00384625.

(ALIE/) ALLEN S M.
(RAFA/) RAFALSKI J A.

Allen SM, Rafalski JA;

WPI; 2003-102520/09.

N-PSDB; AAL53989.

PT Novel ammonium transporter polypeptide useful for identifying enzymatic
inhibitors, which is homologous to corn, soybean, wheat or rice ammonium
transporter polypeptides.

Claim 14; Page 22-23; 27pp; English.

The invention relates to a novel ammonium transporter protein comprising
90% homology based on the Clustal method compared to: a corn ammonium
transporter polypeptide of 183 or 63 amino acids; a soybean ammonium
transporter polypeptide of 500 or 466 amino acids; a wheat ammonium
transporter polypeptide of 494 or 470 amino acids; and a rice ammonium
transporter 497 amino acids fully defined in the specification. The
isolated polynucleotide is useful for selecting an isolated
polynucleotide that affects the level of expression of the ammonium
transporter polypeptide in a plant cell. The ammonium transporter protein
is useful for preparing antibodies which are useful for detecting the
transporter protein in situ in cells or in vitro in cell extracts, and as
targets to facilitate design and/or identify inhibitors of the enzymes
that are useful as herbicides. The isolated polynucleotide is also useful
for creating transgenic plants in which the polynucleotide is present at
higher or lower levels than normal, and for designing and producing
primer pairs which are useful in amplification or primer extension
reactions. This sequence represents the soybean high affinity ammonium
transporter protein of the invention

Sequence 486 AA;

Query Match 73.4%; Score 1860.5; DB 6; Length 486;
Best Local Similarity 71.9%; Pred. No. 6.3e-170;
Matches 341; Conservative 51; Mismatches 77; Indels 5; Gaps 2;

9 PLAYQGNASVADMLKNDAMQVLAATLVGLQSPGLVYL YGCVYKKKVAVNSAFMAL 68
DB 4 PLAYQGNASVADMLKNDAMQVLAATLVGLQSPGLVYL YGCVYKKKVAVNSAFMAL 62
QY 69 YAPAAVVICWVTAAVYNNSPFGEKLPYNGKARPAIDQGLVGRALPATVHYRADGSVETAA 128
DB 63 YAPAAVVICWVTAAVYNNSPFGEKLPYNGKARPAIDQGLVGRALPATVHYRADGSVETAA 122
QY 129 AVEPLYPMATVYFQCVPAATITLIVAGSLGKMSFLAMMI FVPLMLTTSYTYGAFLMG 188
DB 123 AVEPLYPMATVYFQCVPAATITLIVAGSLGKMSFLAMMI FVPLMLTTSYTYGAFLMG 182
QY 189 GGFLEPHMGVIDYCGGVYVHVSAGIAGFTAAVYVGPRAOKRERPPNNILFTLTGAGLLM 248
DB 183 GGFLEPHMGVIDYCGGVYVHVSAGIAGFTAAVYVGPRAOKRERPPNNILFTLTGAGLLM 242
QY 249 MGMAGFNGGPPYANASVAMVAVLNTNICTAMSLIWTCLDVIFFKKPSVAVQGMITGL 308
DB 243 MGMAGFNGGPPYANASVAMVAVLNTNICTAMSLIWTCLDVIFFKKPSVAVQGMITGL 302
QY 309 VCITPAAGVYQGMALVYMGVLAAGSIPTWYTMILHKSKILQVDDTLGVHHTGAVAGLLG 368
DB 303 VCITPAAGVYQGMALVYMGVLAAGSIPTWYTMILHKSKILQVDDTLGVHHTGAVAGLLG 362
QY 369 GILTGLFAEPTLCNLFPLVADSRGAFYGGAGAGOFQKQIAGLFEVYANVNTSLICLAI 428
DB 363 GILTGLFAEPTLCNLFPLVADSRGAFYGGAGAGOFQKQIAGLFEVYANVNTSLICLAI 422
QY 429 NLVPLRMPDDKLEVGDDAVHGEBAAYALMGDGEWYDTVKHS---DAAVAPV 478
DB 423 NLVPLRMPDDKLEVGDDAVHGEBAAYALMGDGEWYDTVKHS---DAAVAPV 476

RESULT 6
AEF16012 standard; protein; 486 AA.

AEF16012;

09-MAR-2006 (first entry)

Glycine max ammonium transporter protein Segid12.

XX ammonium transfer; transgenic plant; nitrogen; cellular transport.
KM Glycine max.
OS US2006010512-A1.
XX 12-JAN-2006.
PD 15-DEC-2004; 2004US-00012668.
PF 28-DEC-2001; 2001US-00033109.
PR (ALIE/) ALLEN S M.
PA (RAFA/) RAFALSKI J A.
XX Allen SM, Rafaleki JA;
PI WPI; 2006-088761/09.
DR N-PSDB; AEF16011.
XX New isolated polynucleotide encoding a polypeptide having ammonium
PT transfer activity, useful for producing transgenic plants with increased
XX nitrogen content.
PS Example 4; SEQ ID NO 12; 29pp; English.
XX This invention relates to a novel isolated polynucleotide encoding a
CC polypeptide having ammonium transfer activity. The polynucleotides are
CC useful for producing transgenic plants with increased nitrogen content.
CC The present sequence is an ammonium transporter protein which is encoded
CC by a nucleotide sequence homologous to the sequence of the invention.
XX
SQ Sequence 486 AA;

Query Match 73.4%; Score 1860.5; DB 10; Length 486;
Best Local Similarity 71.9%; Pred. No. 6.3e-170; Indels 5; Gaps 2;
Matches 341; Conservative 51; Mismatches 77;

QY 9 PLAYOGNTSASVADWLNKGDNAWQVAATLVGLQSVGLVLYGGVKKKMAVNSAFMAL 68
DB 4 PLAYQEHLPAA-PEWLNKGDNAWQVAATLVGLQSVGLVLYGGVKKKMAVNSAFMAL 62
QY 69 YAPAAVWICWTVWYVMSFGKLLPIWGRAPALDGLVGRAPALPATVYHRAAGSVETA 128
DB 63 YAPAAVWICWTVWYVMSFGKLLPIWGRAPALDGLVGRAPALPATVYHRAAGSVETA 122
QY 129 AVEPLTPMATVYVFCVFAATLILVAGSLGRMSFLAMMIFVPLMTFSYTVGAFSLWG 188
DB 123 PEEPPYPMASLYVFPFTFAITLILAGSVLGRMNIKAMMAFVPLMTFSYTVGAFSLWG 182
QY 189 GGFLEFMWIDYDCGVIHVNSAGIAGFTAAVYWGPAOKDRERFPNNILFTLTGAGLIM 248
DB 183 GGFLEFMWIDYDCGVIHVNSAGIAGFTAAVYWGPAOKDRERFPNNILFTLTGAGLIM 242
QY 249 MGNMAGNNGGAPYAANSVASMAVNLNTNICRAMSLIVTCLDIVIEFKKPSVGAQGMITGL 308
DB 243 MGNMAGNNGGAPYAANSVASMAVNLNTNICRAMSLIVTCLDIVIEFKKPSVGAQGMITGL 302
QY 309 VCTTPAAGVYQGAALVYMGVLAGSIWYTMILHRSKILQRPDPTLGVPHHTGAVGLIG 368
DB 303 VCTTPAAGVYQGAALVYMGVLAGSIWYTMILHRSKILQRPDPTLGVPHHTGAVGLIG 362
QY 369 GILTTGFAEPTLCNLFPLVADSRGAFYGGAGAQFGKQIAGLGLFVVAAMVVTSLICLAI 428
DB 363 GILTTGFAEPTLCNLFPLVADSRGAFYGGAGAQFGKQIAGLGLFVVAAMVVTSLICLAI 422
QY 429 NLLVPLRMPDDKLEVGDDAVHGEAAVALMGDGMVYVTKGSGS---DAVAAPV 478
DB 423 NLLVPLRMPDDKLEVGDDAVHGEAAVALMGDGMVYVTKGSGS---DAVAAPV 476

RESULT 7

AAO26536
ID AAO26536 standard; protein; 497 AA.
XX
AC AAO26536;
XX
DT 18-FEB-2003 (first entry)
XX
DE Rice high affinity ammonium transporter protein.
XX
KW Herbicide; ammonium transporter protein; herbicide; transgenic plant;
KM rice.
XX
OS Oryza sativa.
XX
FN US2002142390-A1.
XX
PD 03-OCT-2002.
XX
PF 28-DEC-2001; 2001US-00033109.
XX
PR 28-AUG-1998; 98US-0098248P.
XX
PR 27-AUG-1999; 99US-00384625.
XX
PA (ALIE/) ALLEN S M.
XX (RAFA/) RAFALSKI J A.
PI Allen SM, Rafaleki JA;
XX
XX WPI; 2003-102520/09.
DR N-PSDB; AAL53988.
XX
XX Novel ammonium transporter polypeptide useful for identifying enzymatic
PT inhibitors, which is homologous to corn, soybean, wheat or rice ammonium
PT transporter polypeptides.
XX
PS Claim 14; Page 20-21; 27pp; English.

CC The invention relates to a novel ammonium transporter comprising
CC 90% homology based on the Clustal method compared to: a corn ammonium
CC transporter polypeptide of 183 or 63 amino acids; a soybean ammonium
CC transporter polypeptide of 500 or 486 amino acids; a wheat ammonium
CC transporter polypeptide of 494 or 470 amino acids; and a rice ammonium
CC transporter 497 amino acids fully defined in the specification. The
CC isolated polynucleotide is useful for selecting an isolated
CC polynucleotide that affects the level of expression of the ammonium
CC transporter polypeptide in a plant cell. The ammonium transporter protein
CC is useful for preparing antibodies which are useful for detecting the
CC transporter protein in situ in cells or in vitro in cell extracts, and as
CC targets to facilitate design and/or identify inhibitors of the enzymes
CC that are useful as herbicides. The isolated polynucleotide is also useful
CC for creating transgenic plants in which the polynucleotide is present at
CC higher or lower levels than normal, and for designing and producing
CC primer pairs which are useful in amplification or primer extension
CC reactions. This sequence represents the rice high affinity ammonium
CC transporter protein of the invention

SQ Sequence 497 AA;

Query Match 67.7%; Score 1715.5; DB 6; Length 497;
Best Local Similarity 69.3%; Pred. No. 6e-156;
Matches 312; Conservative 54; Mismatches 83; Indels 1; Gaps 1;

QY 19 SVADWLNKGDNAWQVAATLVGLQSVGLVLYGGVKKKMAVNSAFMALYAPAAVWICW 78
DB 16 AVEPLMTNTGDNWQVAATLVGLQSVGLVLYGGVKKKMAVNSAFMALYAPAAVWICW 75
QY 79 YWMAVMSFGKLLPIWGRAPALDGLVGRAPALPATVYHRAAGSVETAAPVPLPMAT 138
DB 76 YWMAVMSFGKLLPIWGRAPALDGLVGRAPALPATVYHRAAGSVETAAPVPLPMAT 135
QY 139 VVYFQCVFAATLILVAGSLGRMSFLAMMIFVPLMTFSYTVGAFSLWGGGFLFMWGI 198
DB 136 VVYFQCVFAATLILVAGSLGRMSFLAMMIFVPLMTFSYTVGAFSLWGGGFLFMWGI 195

QY DYCGGYVTHVSAGIAGFTAAVWVGPRAOKRERPPNNILFTLTGAGLLMMGMAGFNGGG 258
DB DSGGIVTHLSGIGFTAAVWVGPRLKSDRERSBNILMIAGGLMLMAGFNGGA 255
QY PYAANSVASMALNTNICTAMSLIWTCLDVIFFKKPSVGAVOGMTGLVCITPAGV 318
DB PYAPRITASIVLNTNVSAAASLFTWCLDVIFFGKPSVIGAVOGMTGLVCITPAGLV 315
QY OGMAALVWGLVAGSIPTWTMMILHKRSKILQVDDTLGVFHTHVAAGLLGGLTGLFPAEP 378
DB HTMAAILMGI CGGSLPWFSSMILHKRSALLQKVDTLAVFHTHVAAGLLGGLTGLFPAEP 375
QY TLCLNLFPLVADSRAFFYGAGAGFGKOIAGGLFVVAANNVVTSLICLAINTLVLPRMPD 438
DB DLTAVHTHIPGARGAFFYG-GIAOVGKOIAGALFVVAANNVATTVILGLVLPRLMPD 434
QY DKLEVGDDAVHGEBAVYALMGDEMYDVTKH 468
DB EQLKIGDDAHGEBAVYALMGDEMFDTVRH 464

RESULT 8
AEF16010 standard; protein; 497 AA.

XX AEF16010;
AC AEF16010;
DT 09-MAR-2006 (first entry)
XX Oryza sativa ammonium transporter protein Segid10.
XX ammonium transfer; transgenic plant; nitrogen; cellular transport.
XX Oryza sativa.
XX US2006010512-A1.
XX 12-JAN-2006.
XX 15-DEC-2004; 2004US-00012668.
XX 28-DEC-2001; 2001US-00033109.
XX (AILE/) ALLEN S M.
XX (RAFA/) RAFALSKI J A.
XX Allen SM, Rafaleki JA;
XX WPI; 2006-088761/09.
XX N-PSDB; AEF16009.
XX New isolated polynucleotide encoding a polypeptide having ammonium transfer activity, useful for producing transgenic plants with increased nitrogen content.
XX Example 4; SEQ ID NO 10; 29pp; English.
XX This invention relates to a novel isolated polynucleotide encoding a polypeptide having ammonium transfer activity. The polynucleotides are useful for producing transgenic plants with increased nitrogen content. The present sequence is an ammonium transporter protein which is encoded by a nucleotide sequence homologous to the sequence of the invention.
SQ Sequence 497 AA;

Query Match 67.7%; Score 1715.5; DB 10; Length 497;
Best Local Similarity 69.3%; Pred. No. 6e-156;
Matches 312; Conservative 54; Mismatches 83; Indels 1; Gaps 1;

QY 19 SVADNINKDNAMQVLAATLVGLGVGLVLYGVVKKKAVNSAFMALVFAAVWICW 78
DB 16 AVPEWINTGDNQMQLAAATFVGLQSWPGLVVLVYGIVKKKMAVNSAFMALVYASTLIW 75

QY VTMAVNSFGEKLPINGKAPALDOGLVGRALPATVHYRADGSYETAABEPLYPMAT 138
DB VLVGFRNAFGRLLPFMCKAGALLTEGFLVARASVPATAHGKGALESPTTEPFYBAS 135
QY VVYQCVPAATITLLVAGSLGRMSFLAMMI FVBLMTFSYTVGAFSLMGGLFHWGVI 198
DB MVLQFELAAITLVILAGSLIGRMNIRKAMNAFTPLMLFSYTVCAFSLMGGLFLYQWGI 195
QY DYCGGYVTHVSAGIAGFTAAVWVGPRAOKRERPPNNILFTLTGAGLLMMGMAGFNGGG 258
DB DSGGIVTHLSGIGFTAAVWVGPRLKSDRERSBNILMIAGGLMLMAGFNGGA 255
QY PYAANSVASMALNTNICTAMSLIWTCLDVIFFKKPSVGAVOGMTGLVCITPAGV 318
DB PYAPRITASIVLNTNVSAAASLFTWCLDVIFFGKPSVIGAVOGMTGLVCITPAGLV 315
QY OGMAALVWGLVAGSIPTWTMMILHKRSKILQVDDTLGVFHTHVAAGLLGGLTGLFPAEP 378
DB HTMAAILMGI CGGSLPWFSSMILHKRSALLQKVDTLAVFHTHVAAGLLGGLTGLFPAEP 375
QY DKLEVGDDAVHGEBAVYALMGDEMYDVTKH 468
DB EQLKIGDDAHGEBAVYALMGDEMFDTVRH 464

RESULT 9
ABB92034 standard; protein; 475 AA.

XX ABB92034;
AC ABB92034;
DT 31-MAY-2002 (first entry)
XX Herbicidally active polypeptide SEQ ID NO 1245.
XX Herbicidal; plant; agriculture; herbicide.
XX Arabidopsis thaliana.
XX WO200210210-A2.
XX 07-FEB-2002.
XX 28-AUG-2001; 2001WO-EP009892.
XX 28-AUG-2001; 2001WO-EP009892.
XX (FARB) BAYER AG.
XX Tietjen K, Weidler M;
XX WPI; 2002-269010/31.
XX Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms.
PS Claim 5; SEQ ID NO 1245; 26pp + Sequence Listing; English.

CC The invention relates to identifying target proteins (ABB90790-ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an E-value greater by a factor of 3 than the E-value of most similar non-plant sequences are selected. CC The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are useful as

CC herbicides
 XX Sequence 475 AA:
 SQ

Query Match 66.4%; Score 1682.5; DB 5; Length 475;
 Best Local Similarity 66.8%; Pred. No. 8,4e-153;
 Matches 300; Conservative 61; Mismatches 77; Indels 11; Gaps 1;

QY 20 VADMLNKGNDAQOLVAATLVGLQSPGLVYLGGVKKKNAVNSAFALYAFPAALVWICWY 79
 DB 12 VPEMLNKGNDAQOLVAATLVGLQSPGLVYLGGVKKKNAVNSAFALYAFPAALVWICWY 71
 QY 80 TMAVNSAFEGEKLPIWGKARPAIDQGLVGRALPATVHVRADGSVETAAVEDELYPMATV 139
 DB 72 LICYKNAFGEELLPWGKGPAPDQGLYKQQAIP-----NSVVAAPFPFPAATL 120
 QY 140 VYFCVFAATTLTLVAGSLGRMSFLAMVIFVPLMLFTSYTGAFFSLMGGFLPHWGVID 199
 DB 121 VYFQTFPAATTLTLVAGSVLGRNLIKAMAFVPLMLFSTTVGAYSLMGGFLYQKGVID 180
 QY 200 YCGGYIVHSAGIAGFTAAVVGPPRAQKDRERFPNNILFTLTGAGLLMNGAGFNGGCP 259
 DB 181 YSGGYVIHLSGVAGFVAATVWGPFRKADREPPNNVILMLAGAGLLMNGMGSGFNGCAP 240
 QY 260 YAANSVASMAYVNTNICTMSLTVWTCIDVIFPKKDSVVGAGVGMITGLVCITPAAGVQ 319
 DB 241 YAANLTSIAVNTNLSAATSLVWTTLDVIFGKDSVIGALQSMVTLGAVTPGAGLIQ 300
 QY 320 GMAALVGVLAGSIPLYTMMILHRSKILQVVDTLGVFHTHGVAGLLGLTGLFAEPT 379
 DB 301 TMAAIIIGVVSCTAPASAMIIHKKSALLQKDDTLAVFTTHAVAGLLGSGIMTGLFAHP 360
 QY 380 LCNLFPLVADSRGAFYGGAGCAQFGKOIAGGLFVAVANNVVTSLICLAINLVLPLMPDD 439
 DB 361 LCVLVLPLPATRGAFYGGNGKQLKQIAGAFIAVNVSTIILAIHVFIPLMAEE 420
 QY 440 KLEVGDDAVHGEERAVYLMGDEMYDVYTKH 468
 DB 421 ELGIGDDAAHGEERAVYLMGDEKFDATRH 449

RESULT 10
 ABM87942
 ID ABM87942 standard; protein; 325 AA.
 AC ABM87942;
 XX
 DT 02-JUN-2005 (first entry)
 DE Rice abiotic stress responsive polypeptide SEQ ID NO:6188.
 KW abiotic stress tolerance; transgenic plant; plant; cereal; agriculture.
 XX
 OS Oryza sativa.
 XX
 PN WO2003008540-A2.
 PD 30-JAN-2003.
 XX
 PF 21-JUN-2002; 2002WO-US019668.
 PR 22-JUN-2001; 2001US-0300112P.
 PR 24-AUG-2001; 2001US-0314662P.
 PR 26-SEP-2001; 2001US-0325277P.
 PR 21-NOV-2001; 2001US-0332132P.
 XX
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 XX
 PI Kreps J, Briggs SP, Cooper B, Glazebrook J, Goff SA, Katagiri F;
 PI Moughamer T, Provart N, Rieke D, Zhu T;
 XX
 DR WPI; 2003-248011/24.

PT New stress-responsive nucleic acid, useful for altering the
 PT responsiveness of a plant, e.g. cereal, to an abiotic stress such as cold
 PT stress, salt stress or osmotic stress.
 XX
 XX Claim 1; SEQ ID NO 6188; 89pp; English.
 PS
 XX
 CC The invention relates to novel abiotic stress responsive polynucleotides
 CC and polypeptides. Also disclosed are vectors, expression cassettes, host
 CC cells, and plants containing such polynucleotides. Also disclosed are
 CC methods for using the polynucleotides and polypeptides to alter the
 CC responsiveness of a plant to abiotic stress. The invention is useful in
 CC agriculture. The nucleic acid is useful for determining whether a test
 CC plant has been exposed to an abiotic stress condition. It is also useful
 CC for selecting an agent that alters abiotic stress regulated
 CC polynucleotide expression in a plant cell, and to identify a homolog or
 CC ortholog to an abiotic stress responsive polynucleotide. The nucleic acid
 CC molecule and the polypeptide encoded by it are useful in altering the
 CC responsiveness of a plant to an abiotic stress, such as cold stress, salt
 CC stress, osmotic stress or any of their combinations. The present sequence
 CC is used in the exemplification of the invention

QY 1 MSSSATVPLAYQGNSTASVADMLNKGNDAQOLVAATLVGLQSPGLVYLGGVKKKNA 60
 DB 1 MSGDAFNMSVAVQPSGMA-VPEWLNKGNDAQOMISATLVQMSVPLVILYGSIVKKKNA 59
 QY 61 VNSAFALYAFPAALVWICWYTWAVNMSFGEKLPIWGKARPAIDQGLVGRALPATVH- 119
 DB 60 VNSAFALYAFPAALVWICWYTWGNMSFGKLLPFWKARPAIDQGLVGRALPATVH- 119
 QY 120 ---RADGSVETRAVEPLYPMATVYVFGCVFAATTLTLVAGSLGRMSFLAMVIFVPLMW 175
 DB 120 KGGGADALVEFTRVWVPLYPMATVYVFGCVFAATTLTLVAGSLGRMSFLAMVIFVPLMW 179
 QY 176 TFSYTVGAFSLWGGFLFHMGYIDYCGYIVHSAGIAGFTAAVVGPPRAQKDRERFPN 235
 DB 180 TFSYTVGAFSLWGGFLFHMGWVMDYSGYVIHLSGVAGFTAAVVGPPRSTDRERFPN 239
 QY 236 NIIFFITGAGLLMNGAGFNGGFPYANSVASMAYVNTNICTMSLIVWTCIDVIFPKKP 255
 DB 240 NVILMLTGAAILMNGAGFNGGDPYSANIDSIAVNTNICAATSLVWTCIDVIFPKKP 299
 QY 296 SVYGAVOGMITGLVCITPAAGVQ 319
 DB 300 SVYGAVOGMITGLVCITPAAGVQ 323

RESULT 11
 ABM90348
 ID ABM90348 standard; protein; 325 AA.
 AC ABM90348;
 XX
 DT 02-JUN-2005 (first entry)
 DE Rice abiotic stress responsive polypeptide SEQ ID NO:9070.
 KW abiotic stress tolerance; transgenic plant; plant; cereal; agriculture.
 XX
 OS Oryza sativa.
 XX
 PN WO2003008540-A2.
 PD 30-JAN-2003.
 XX
 PF 21-JUN-2002; 2002WO-US019668.
 PR 22-JUN-2001; 2001US-0300112P.

PR 24-AUG-2001; 2001US-0314662P.
PR 26-SEP-2001; 2001US-0325277P.
PR 21-NOV-2001; 2001US-0332132P.
XX
XX (SYGN) SYNGENTA PARTICIPATIONS AG.
XX
XX Krepes J, Briggs SP, Cooper B, Glazebrook J, Goff SA, Katagiri F;
PI Moughamer T, Provart N, Ricke D, Zhu T;
XX WPI; 2003-248011/24.
XX
XX New stress-responsive nucleic acid, useful for altering the
PT responsiveness of a plant, e.g. cereal, to an abiotic stress such as cold
PT stress, salt stress or osmotic stress.
XX
XX Claim 1; SEQ ID NO 9070; 89pp; English.
XX
XX The invention relates to novel abiotic stress responsive polynucleotides
CC and polypeptides. Also disclosed are vectors, expression cassettes, host
CC cells, and plants containing such polynucleotides. Also disclosed are
CC methods for using the polynucleotides and polypeptides to alter the
CC responsiveness of a plant to abiotic stress. The invention is useful in
CC agriculture. The nucleic acid is useful for determining whether a test
CC plant has been exposed to an abiotic stress condition. It is also useful
CC for selecting an agent that alters abiotic stress regulated
CC polynucleotide expression in a plant cell, and to identify a homolog or
CC ortholog to an abiotic stress responsive polynucleotide. The nucleic acid
CC molecule and the polypeptide encoded by it are useful in altering the
CC responsiveness of a plant to an abiotic stress, such as cold stress, salt
CC stress, osmotic stress or any of their combinations. The present sequence
CC is used in the exemplification of the invention
XX
XX Sequence 325 AA;
SQ
Query Match 53.6%; Score 1357; DB 7; Length 325;
Best Local Similarity 76.5%; Pred. No. 1.1e-121;
Matches 248; Conservative 30; Mismatches 40; Indels 6; Gaps 2;
QY 1 MESSATVPLVAGTNSASVADMLKGDNAQVLAATVGLQSVPLVLYGCVKKKA 60
DB 1 MSGDANMSVAVQPSGMA-VPEWLKNGDNAMQWISITLVGMSVPLVLYGSIYKKKA 59
QY 61 VNSAFALYAFAPAVMTCWTTNAYNMSFGEKLPFGKARPALDOGLVGRALPATVHY- 119
DB 60 VNSAFALYAFAPAVMTCWTTNAYNMSFGEKLPFGKARPALDOGLVGRALPATVHY- 119
QY 120 ----RADGSVETAAVEPLYPMATVVFQCVFAITLILVAGSLIGRMSFLANMIFVPLWL 175
DB 120 KGGGADALVERPFWVPLYPMATVVFQCVFAITLILVAGSLIGRMSFLANMIFVPLWL 179
QY 176 TTSYTYGASLWGGGLFHWGVLDYCGGYIHSAGIAGFTAAVWGPRAQKDRERFPN 235
DB 180 TTSYTYGASLWGGGLFHWGVLDYCGGYIHSAGIAGFTAAVWGPSTXDRERFPN 239
QY 236 NTLFRTLGLMLMAGAFNGGFPYANASVAMVNTNICTAMSLIWTCTDVIFFKKP 295
DB 240 NVLLMLTGLMGLMAGAFNGGFPYANASVAMVNTNICTAMSLIWTCTDVIFFKKP 299
QY 296 SVVGAQGMITGLVCTTPAAGVQ 319
DB 300 SVVGAQGMITGLVCTTPAGVQC 323
RESULT 12
ABM89810
ID ABM89810 standard; protein; 440 AA.
XX
XX ABM89810;
AC
XX 02-JUN-2005 (first entry)
DT
XX
DE Rice abiotic stress responsive polypeptide SEQ ID NO:8056.
XX

KW abiotic stress tolerance; transgenic plant; plant; cereal; agriculture.
XX
XX Oryza sativa.
OS
XX WO2003008540-A2.
XX
XX
XX 30-JAN-2003.
PD
XX 21-JUN-2002; 2002MO-US019668.
PF
XX
XX 22-JUN-2001; 2001US-0300112P.
PR 24-AUG-2001; 2001US-0314662P.
PR 26-SEP-2001; 2001US-0325277P.
PR 21-NOV-2001; 2001US-0332132P.
XX
XX (SYGN) SYNGENTA PARTICIPATIONS AG.
XX
XX Krepes J, Briggs SP, Cooper B, Glazebrook J, Goff SA, Katagiri F;
PI Moughamer T, Provart N, Ricke D, Zhu T;
XX WPI; 2003-248011/24.
XX
XX New stress-responsive nucleic acid, useful for altering the
PT responsiveness of a plant, e.g. cereal, to an abiotic stress such as cold
PT stress, salt stress or osmotic stress.
XX
XX Claim 1; SEQ ID NO 8056; 89pp; English.
XX
XX The invention relates to novel abiotic stress responsive polynucleotides
CC and polypeptides. Also disclosed are vectors, expression cassettes, host
CC cells, and plants containing such polynucleotides. Also disclosed are
CC methods for using the polynucleotides and polypeptides to alter the
CC responsiveness of a plant to abiotic stress. The invention is useful in
CC agriculture. The nucleic acid is useful for determining whether a test
CC plant has been exposed to an abiotic stress condition. It is also useful
CC for selecting an agent that alters abiotic stress regulated
CC polynucleotide expression in a plant cell, and to identify a homolog or
CC ortholog to an abiotic stress responsive polynucleotide. The nucleic acid
CC molecule and the polypeptide encoded by it are useful in altering the
CC responsiveness of a plant to an abiotic stress, such as cold stress, salt
CC stress, osmotic stress or any of their combinations. The present sequence
CC is used in the exemplification of the invention
XX
XX Sequence 440 AA;
SQ
Query Match 53.4%; Score 1352; DB 7; Length 440;
Best Local Similarity 63.1%; Pred. No. 5.1e-121;
Matches 253; Conservative 45; Mismatches 59; Indels 44; Gaps 4;
QY 106 LTVGRALPA-TVHYRADGSVETAAVEPLYPMATVVFQCVFAITLILVAGSLIGRMSF 164
DB 24 LTVGRALPA-TVHYRADGSVETAAVEPLYPMATVVFQCVFAITLILVAGSLIGRMSF 164
QY 165 LAMTIFVPLMIFSTYVGAFAFSLWGGGLFHWGVLDYCGGYIHSAGIAGFTAAVWGP 224
DB 78 KAMAFVPLMIFSTYVGAFAFSLWGGGLFHWGVLDYCGGYIHSAGIAGFTAAVWGP 137
QY 225 AOKDRERFPNNILFTLGLGLMAGAFNGGFPYANASVAMVNTNICTAMSLIWT 284
DB 138 SASDRERFPNNILFTLGLGLMAGAFNGGFPYANASVAMVNTNICTAMSLIWT 197
QY 285 TGLDVIFFPKKPSVGAQGMITGLVCTTPA-----GVVQGW--- 321
DB 198 TGLDVIFFPKKPSVGAQGMITGLVCTTPA-----GVVQGW--- 321
QY 322 -----AALVWGLAGSIPLYTMMILHKRSKILQRYVDTLGVFTTHVAGLL 367
DB 258 LVCITPAGAPGARLAIYMGILSGSIPYTTMMVHLKKMSFMRIDDTLGVFTTHVAGRL 317
QY 368 GGLLTGLFAEPTLCNLFPLVADSRGAFYGGAGAGFGQIAGGLFVVAANVYVSLICLA 427
DB 318 GGATYGLFAEPTLCNLFPLVADSRGAFYGGAGAGFGQIAGGLFVVAANVYVSLICVI 377

CC responsiveness of a plant to an abiotic stress, such as cold stress, salt
CC stress, osmotic stress or any of their combinations. The present sequence
CC is used in the exemplification of the invention
XX
SQ Sequence 476 AA;
Query Match 27.4%; Score 693.5; DB 7; Length 476;
Best Local Similarity 36.4%; Pred. No. 1.4e-57;
Matches 170; Conservative 73; Mismatches 173; Indels 51; Gaps 10;
QY 2 SSSATVTVPLAYOGNTSAS----VADWLNKGDNAQVLAATLVGLQSVGLVVLGVVK 56
Db 45 SESVAVEELHDAAPAAAPAAVAEAAAADRGDAVAMMLSTLLVLMVPGALPFGGLVR 104
QY 57 KKMVNSAFMALYAAPAAVWCMTAAVYNNMSFEKLLPIWGKRRPDLQGLVGRALPRT 116
Db 105 SKNVLSVLSQILVSVLSVLVLLMWAVGSAVFSAG-NPFPGS---FTEFAFLKG----- 153
QY 117 VHYRADGSVETAAVEPLVMATVVFQCVFAITLILVGLSLLGMSFLAMWIFVPLMLT 176
Db 154 --FTPD-SVGNTPPIKGL-PDYLFVAFQSTFAGITTLIYGAFAERIKFPAVLIFGALMFT 209
QY 177 FSYTVGAFSLWGGGFLFHWGVVIDYCGVYIVHSAGIAGFTAAVWVGPRAQKDERFPNN 236
Db 210 LSYIPMAHIVMGGYLIGELGALDPAGGTVTHINAGVAGVFGKRLGYQGTALKEPHN 269
QY 237 ILFLTIGAGLLMGNAAGRGGSPYAANSVAAVNTNICTMSLIVTCLDVIFFKPRS 296
Db 270 VPFTYIGAMLVWVGFGFAGSAADAVASLAFNTVLTAAVLAQWLTVBAIKGRPS 329
QY 297 VVGAQVQGITGLVCTTPAAGVVGWMAALVGVLAGISIPYTMILHKSKILQRYDDTLG 356
Db 330 ALGAASGAVAGLVGITTPAGCTVGPGLGAIYIGFVAGVVCWVGTLG----KLLKXDDTD 385
QY 357 VFHTHGVAGLLGGLLTGLFAEPTLCNLFPLVADSAGAFYGAAGAFQKQIAGLFLV--- 413
Db 366 VFGVGVGIVGAILTGVFSAGSL-----GGTKADLDLDAHQVWVQV 427
QY 414 -----VANNVVTSLICLAINLLVPLRMDDKLEVGDDAV-HGEERAY 454
Db 428 SVGLTVLMSAVVTAVILLVVKVVGRLVTEAERTGLDVTSHGESAY 474
RESULT 15
ABBS4938
ID ABBS4938 standard; protein; 413 AA.
XX
AC ABBS4938;
XX
DT 29-AUG-2003 (revised)
XX
DT 16-MAY-2002 (first entry)
XX
DE Lactococcus lactis protein amtb.
XX
KM Bioethesis; biodegradation; lactic bacterium; yogurt; cheese.
XX
OS Lactococcus lactis; IL1403.
XX
FN FR2807446-A1.
XX
PD 12-OCT-2001.
XX
PE 11-APR-2000; 2000FR-00004630.
XX
PR 11-APR-2000; 2000FR-00004630.
XX
PA (INRG) INRA INST NAT RECH AGRONOMIQUE.
XX
PI Bolotine A, Sorokine A, Renault P, Ehrlich SD;
XX
DR WPI, 2002-043418/06.
XX
PT New nucleotide sequence useful in the identification or Lactococcus

PT Lactis and related species.
XX
PS Claim 6; SEQ ID NO 1640; 2504pp; French.
XX
XX The present invention is related to a Lactococcus lactis nucleotide
CC sequence (ABA90521) and related proteins (ABBS3300-ABBS5621). The nucleic
CC acid sequence is useful in the detection and/or amplification of nucleic
CC acid sequence, particularly to identify Lactococcus lactis or related
CC species. The proteins of the invention are useful for the biosynthesis or
CC biodegradation of a composition of interest. The invention helps research
CC in lactic bacteria, particularly useful in the production of yogurt and
CC cheese. Note: The sequence data for this patent is based on equivalent
CC patent WO200177334 (published 18-OCT-2001) which is available in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences. (Updated on 29-AUG-2003 to
CC standardise OS field)
XX
SQ Sequence 413 AA;
Query Match 25.7%; Score 652; DB 5; Length 413;
Best Local Similarity 34.0%; Pred. No. 1.2e-53;
Matches 150; Conservative 72; Mismatches 173; Indels 46; Gaps 9;
QY 24 LNKGDNAMQVLAATLVGLQSVGLVVLGVKKKMAVNSAFMALYAPAAVWCMTWAY 83
Db 1 MDTSIAFLICALVFLMT-PALAFYGGIGRRKRVNLTWMSGLAPWALASILMIIGF 59
QY 84 NMSFEKLLPIWGKRRPDLQGLVGRALPRTVHYRADGSVETAAVEPLPMAV----- 139
Db 60 SFSFS-----GNSWIGDFHILFPMNGVDMAK-NSLPPANHIDGL 98
QY 140 -VYFQCVPAITLILVAGSLGRMSFLAMWIFVPLMLTFSYTVGAFSLWGGGFLFHWGV 198
Db 99 FSGFQMMISITVALITSVVGKRRFTPIILFPMKMLLVYPLAHMWGGGFLAQIHAI 158
QY 199 DYCGGVYIVHSAGIAGFTAAVWVGPRAQKDERFPNNILFTLGAGLLMGMAGFNGGG 258
Db 159 DPAGGDVHHISSGVTGLGALVLVGRKRDYERLDVRPHNIPVVLGAGLLMFGMFGFNAGS 218
QY 259 PYAANSVAAVNTNICTMSLIVTCLDVIFFKPRSVAAGVGMITGLVCITPAAGV 318
Db 219 ALAANGVAINAFMTNTTAAAMAFSMTIVEKILIGKPSIVAGCSGAVVGLVAITPAGAFV 278
QY 319 QGMALVWGVLAGSIPYTMILHKSKILQRYDDTLGVFHTHGVAGLLGGLTGLFAEP 378
Db 279 SLMSLLIIGLVSPUSYPMISVKKK---LGYDALLDAFGCHGIGMFGIMTGFATP 334
QY 379 TLCNLFELVADSRGAFYGAAGAFQKQIAGLFPVANNVVTSL---ICLAINLVPL 434
Db 335 ALA-----PEKGYAGLIVGS-----GKLLANVSAVVFVIFALVSWIILKVIALFMP 384
QY 435 RMPDDKLEVG-DDAVHGEERAY 454
Db 385 RVSDBRAEAIGLDSEHEETAY 405

Search completed: July 22, 2006, 03:27:53
Too time : 201 secs

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OM protein - protein search, using sw model

Run on: July 22, 2006, 03:28:11 ; Search time 41 Seconds
(without alignments)
1124.093 Million cell updates/sec

Title: US-10-713-648A-63

Perfect score: 2534
Sequence: 1 MESSATVPLAYQGNISASV.....GEMVDYTKGSDAAVAPVV 479

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1682.5	66.4	475	2	T01260
2	985.5	38.9	509	2	G90257
3	722	28.5	412	2	C69188
4	717.5	28.3	442	2	C82985
5	706	27.9	433	2	H70310
6	691	27.3	431	2	AF0381
7	660	26.0	428	2	AC0560
8	659	26.0	433	2	AB3273
9	655.5	25.9	439	2	B75487
10	652	25.7	433	2	H86823
11	651.5	25.7	510	2	C87415
12	650.5	25.7	492	2	AB2632
13	650	25.7	428	2	E85542
14	650	25.7	428	2	C64775
15	650	25.7	428	2	A90692
16	640.5	25.3	407	2	A69188
17	637.5	25.2	404	2	A36865
18	635.5	25.1	434	2	C81927
19	633.5	25.0	477	2	H70747
20	632.5	25.0	434	2	E81177
21	621	24.5	449	2	H97689
22	621	24.5	449	2	AE2915
23	619	24.4	470	2	AE1930
24	591.5	23.3	401	2	AF1266
25	589.5	23.3	401	2	AD1264
26	589	23.2	416	2	A89996
27	582.5	23.0	448	2	T35667
28	574.5	22.7	391	2	A69372
29	569.5	22.5	405	2	H96983

30	567	22.4	388	2	D69468	ammonium transport
31	515	20.3	510	2	E82918	ammonium transport
32	513.5	20.3	512	2	T50244	probable ammonium
33	507.5	20.0	521	2	F82918	ammonium transport
34	506	20.0	499	2	S51089	ammonium transport
35	474.5	18.7	492	2	S46225	ammonium transport
36	451.5	17.8	489	2	S69027	ammonium transport
37	448.5	17.7	435	2	H72379	ammonium transport
38	425.5	16.8	421	2	B84129	ammonium transport
39	410.5	16.2	507	2	S76687	hypothetical prote
40	405	16.0	518	2	AD1930	ammonium transport
41	384	15.2	442	2	S74801	ammonium transport
42	372	14.7	468	2	A69468	ammonium transport
43	357	14.1	498	2	AC1930	ammonium transport
44	338.5	13.4	501	2	T06653	ammonium transport
45	337.5	13.3	514	2	T06585	ammonium transport

ALIGNMENTS

```
RESULT 1
T01260
probable ammonium transport protein F16M14.22 - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C/Accession: T01260; T02516; B84603
R/Rounsfley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.
submitted to the EMBL Data Library, July 1998
A/Description: Arabidopsis thaliana chromosome II BAC T19C21 genomic sequence.
A/Reference number: Z14213
A/Accession: T02516
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-475 <R0U>
A/Cross-references: UNIPROT:Q9M6N7; UNIPARC:UPI0000048613; EMBL:AC003028; NID:G3335356; I
R/Rounsfley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul,
submitted to the EMBL Data Library, August 1998
A/Description: Arabidopsis thaliana chromosome II BAC T19C21 genomic sequence.
A/Reference number: Z14676
A/Accession: T02516
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-434 <R02>
A/Cross-references: UNIPARC:UPI0000178B16; EMBL:AC004683; NID:G3395421; PID:G3395443
A/Experimental source: cultivar Columbia
R/Rlin, X.; Kaul, S.; Rounsfley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
Nature 402, 761-768, 1999
A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A/Reference number: A84420; WUID:20083487; PMID:10617197
A/Accession: B84803
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-475 <STO>
A/Cross-references: UNIPARC:UPI0000048613; GB:AE002093; NID:G6598436; PIDN:AA28754.2; G
C/Genetics:
A/Map position: 2
A/Intons: 104/3; 201/3; 297/1; 331/3
C/Superfamily: ammonium transporter nrgA

Query Match      66.4%; Score 1682.5; DB 2; Length 475;
Best local similarity 66.8%; Pred. No. 3.1e-121;
Matches 300; Conservative 61; Mismatches 77; Indels 11; Gaps 1;
```

```
Db 72 LUCYMGARBEELLPEPMKCGRAFDGCVLKGAKIP-----NSVNAPEPMTL 120
Oy 140 VFQCVFAATITLILVAGSLGRMSFLAMNI FVPLMTESYTVGAPSLMGCGFLFHWGVID 199
Db 121 VFQCFPAITITLILVAGSLGRMNIKAWMA FVPLMTIFSYTVGAYSIMGGGLYOMGVID 180
Oy 200 YCGGVVHVSAGIAGTAAYWVGPRACKRERFPNNILFTLTGAGLLMGAGNCGGP 259
Db 181 YSGGVVHVSAGIAGTAAYWVGPRACKRERFPNNILMTLAGGLMGMSGENCGAP 240
Oy 260 YAANSVSAVANTNICTAMSLIWTCLDVIFEKPSVVGAVOGMITGLVCTTPAAVQ 319
Db 241 YAANLTSSIAVANTNLSATSLTWTTLDVIFPGKRSVIGALQGMVGTAGAVTPGAGLIQ 300
Oy 320 GHAALVMGYLAGSIPTWYTMILHKSKILQVDDTLGVHTHGVAGLLGGLTGLFAERT 379
Db 301 TMAAIIIGVSGTAPASWMIHKKSALLQKVDTLAVFYTHAVVAGLLGGLTGLFAHPD 360
Oy 380 LCNLEFVADSRGAFYGGAGAGQFOGKQIAGL FVYAMNVVTSICLATINLVLRLMPD 439
Db 361 LCVLVLPLPATGAFYGGAGQQLKQLGAAPFIAMNVSTTILILALRVFPLRMABE 420
Oy 440 KLEVGDDAVHGEBAAYALMGDGMVDYTKH 468
Db 421 ELGIGDDAHGEBAYALMGDGEKFDATRH 449
```

RESULT 2

```
G90257
ammonium transporter SSO1054 [imported] - Sulfolobus solfataricus
C,Species: Sulfolobus solfataricus
C,Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C,Accession: G90257
R,She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-
Jong, I.; Jeffries, A.C.; Kozere, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, F.
arrett, R.A.; Regan, M.A.; Sersen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A,Description: Sulfolobus solfataricus complete genome.
A,Reference number: A99139
A,Accession: G90257
A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-509 <KUR>
A,Cross-references: UNIPROT:Q97275; UNIPARC:UPI0000064334; GB:AE006641; NID:G13814242; F
C,Genetics:
C,Superfamily: ammonium transport protein
```

Query Match 38.9%; Score 985.5; DB 2; Length 509;

Best Local Similarity 44.7%; Pred. No. 7.1e-68;

Matches 203; Conservative 63; Mismatches 143; Indels 45; Gaps 8;

```
Oy 17 SASVADMLKGNDAQVLAATLVGLQSVGLVVLXGVVKKKMAVNSAFMALYAPAAWI 76
Db 56 AAASVMDLTGSAMMLTATFGLQSVGVALLVYAGLSKKKXAVNSALMIFAPAAVLV 115
Oy 77 CVATTAAYNMSFGKLL-----PIWGKAPALDOGLVGRAL--PATYHYA 121
Db 116 IWIINGVSFGFPAVLSIHGYIGFYPIPWG-----GLFEASQTTVYGGSGAHAN- 166
Oy 122 DGSVERAAVEPLYPMAVTVYFQCVFAATITLILVAGSLGRMSFLAMNIFVPLMTESYTV 181
Db 167 -----LPTATFFQCFPAITITLILVAGSLGRMNFKAMNVVFPMSLLVISP 214
Oy 183 GAFSLMGCGFLFHWGVIDYCGGVVHVSAGIAGTAAYWVGPRACKRERFPNNILFTL 241
Db 215 VAYWLPAGGWLINGAVDSGGVYHVDAVGALLAALAIIGPLASER-KLEAHSPLVL 273
Oy 242 TGAAGLIMAGPANGGAPPAANSVASMAVLTNTICTAMSLIYVTCIDVIFPKKPSVGVAV 301
Db 274 VAGGLIMGMDGNGDPLGATVDAAI AVLNTNITATVAVVAMVLMDMKRFQGPPTLIGAT 333
```

```
Oy 302 QGMITGLVCTTPAAGVVGMAALVMGYLAGSIPTWYTMILHKRSKILQVDDTLGVFPTH 361
Db 334 SGATITGLVAITPAGVYVNGWABALIGIFSSGSIIPMALYWEPRK----LRVDDTLGVSTH 389
Oy 362 GVAGLIGGLTGLTGLFAEPTLCNLFLPVADSRGAFYGGAGAGQFOGKQIAGGLFVYAMNVTV 421
Db 390 GIAGIVGGLTGVFANPANTVQFVAP--GLTGALYG--NWQLGIOALAAVIVFYVDFAIT 445
Oy 422 SLICLATINLVLRLMPDDKLEVGDDAVHGEBAAYA 455
Db 446 FGLKFTIGLFLPLQAPQELAIQDYAHMGEBAVYS 479
```

RESULT 3

```
C69188
ammonium transporter - Methanobacterium thermoautotrophicum (strain Delta H)
C,Species: Methanobacterium thermoautotrophicum
C,Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C,Accession: C69188
R,Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; E
; Qiu, D.; Spadefora, R.; Viccare, R.; Wang, Y.; Mierzowaki, J.; Gibson, R.; Jiwani, N.
; K.; Church, G.M.; Daniels, C.U.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A,Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: functi
A,Reference number: A69000; MUID:98037514; PMID:9371463
A,Accession: C69188
A,Status: preliminary; nucleic acid sequence not shown; translation not shown
A,Molecule type: DNA
A,Residues: 1-412 <MTH>
A,Cross-references: UNIPROT:O26759; UNIPARC:UPI000013989C; GB:AE000846; GB:AE000666; NID:
A,Experimental source: strain Delta H
C,Genetics:
C,Superfamily: ammonium transporter nrgA
```

Query Match 28.5%; Score 722; DB 2; Length 412;

Best Local Similarity 36.6%; Pred. No. 8.3e-48;

Matches 159; Conservative 74; Mismatches 169; Indels 32; Gaps 7;

```
Oy 24 LNKGDNAQVLAATLVGLQSVGLVVLXGVVKKKMAVNSAFMALYAPAAWICMVTWY 83
Db 10 LNSGDTAMMLVSTALVMTVPGVALFYGLTKKENVLTMTFSLIAFAVTSITLVLYG 69
Oy 84 NMSFGKLLPIWGKAPALDOGLVGRALPATYHYRADGSVERAAVEPLYPMAVTVYQ 143
Db 70 QPABADLMGFGSPVNLMMGVGNTA-----AALAPTPDPFLYIAFQ 113
Oy 144 CVFAATITLILVAGSLGRMSFLAMNIFVPLMTESYTVGAPSLMGCGFLFHWGVIDYCGG 203
Db 114 LTFATITVALISGAVVERMKFSAMLAFLVLSVYVVAHVMWGGGFLAQLGALDFAGG 173
Oy 204 YVHVSAGIAGTAAYWVGPRACKRERFPNNILFTLTGAGLLMGAGNCGGPYAN 263
Db 174 TVVHINSVGAALAVVLLGKR--KD--TRLPLNIGSYIGASLMLFGFGFNAGSALTAG 230
Oy 264 SVASAAVANTNICTAMSLIWTCLDVIFEKPSVVGAVOGMITGLVCTTPAAGVQMAA 323
Db 221 GLAASAFVLTNTTAAAGAVSVIMDYLVKGRFVYLGISGAVAGVATTPAAGFTVPA 290
Oy 324 LVMGYLAGSIPTWYTMILHKSKILQVDDTLGVHTHGVAGLLGGLTGLFAEPTLCNL 383
Db 291 LIIGLVTSIVISLAVSYLKP---LGYDDALDVFGLMGISGVSATGLFAAPFINEL 346
Oy 384 FLPVADSRGAFYGGAGAGQFOGKQIAGL FVYAMNVVTSICLATINLVLRLMP--DDTLR 442
Db 347 -----GTGLLYGNB--QLTAQVIAVAVVAVSVVTLILIGKLDFVGLVSGKEEWE 398
Oy 443 VGDDAVHGEBAAYAL 456
Db 399 GLDTHLHRETYRI 412
```

RESULT 4

C82985
ammonium transporter AmtB PA5287 [imported] - Pseudomonas aeruginosa (strain PA01)
C/Species: Pseudomonas aeruginosa
C/Date: 15-Sep-2000 #sequence_rev150n 15-Sep-2000 #text_change 09-Jul-2004
C/Accession: C82985
R/Stover, C.K.; Pham, X.Q.; Ewitt, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Badian, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kae, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A/Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen
A/Reference number: A82950; NCID:20437337; PMID:10984043
A/Accession: C82985
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-442 <STO>
A/Cross-references: UNIPROT:Q9HTR7; UNIPARC:UPI000000C5F8B; GB:AE004941; GB:AE004091; NID: A;Experimental source: strain PA01
C/Genetics:
A/Gene: amtB; PA5287
C/Superfamily: ammonium transporter nrgA

Query Match 28.3%; Score 717.5; DB 2; Length 442;
Best Local Similarity 36.7%; Pred. No. 2e-47;
Matches 170; Conservative 70; Mismatches 178; Indels 45; Gaps 10;

QY 7 VVPLAQNTSASVADMLKKGDNAQVATVYGLQSVPGVLYGCVVKKKAAVNSAFM 66
DB 12 LLSLALPGVALAEEBVLNSGDTAMMLISALVLTMTIPGLALFYGGMVPAK-NVLSIMM 70
QY 67 ALYAFAPA-WVICVNTAANNYSFG-----EKLPIWKGARPALDQGLLVGRALPATVHYRA 121
DB 71 QCFATITGLTITLVVYGYSLAFPTAGMEKVLNFSFVGGLDRAFLSG-----LRA 121
QY 122 DGSVETAAVEPLYPATVVFQCFAPATLTLIVAGSLIGMSPLAMMIFVPLMTFSYTV 181
DB 122 DGTSTATA---LPPESVITFTQMTFALITPALLVGAFAERMKFSAMLIEMAVFTVYAP 178
QY 182 GAESLWG--GGFLFHGVIDYCGGYVTHSAGIAGTAAVYVGPRAQKREPPNNILF 239
DB 179 IAHMVWSGCGALMWDGVLDFAGGTVHHVAGIAGVACLVIGKRKGYPTTPMAPHNLGY 238
QY 240 TLTVAGLLMWMGAFNGGCGPYAANSVASMAVLNTNICTAMSLIWTCLDVIFFKXPSVVG 239
DB 239 TLVGAALMLTMGMFGFAGSAAANNGTRGAMLVTOJATAAALAMFAEITHTGKPSALG 238
QY 300 AVQGMITGLVCTTPAAGVVOGMALVMGVLAGSIPWTWMLIHKRSKILQRPVDTLGVPH 359
DB 299 IASGVVAGVATTPAAGTAGPMGALVIGLASVITCFPAATSLKRAK---YDSDDAFG 354
QY 360 THGVAGLLGGLLTGLFAEPTLCNLFLPVADSRGAFYGGAG---GAQFSQIAGLGFV 414
DB 355 VHAVGVIGVALLTGLFPAAPSL-----GGFSGVSDIGAQFVQKGVAFV 399
QY 415 AMNVVYTSLICLAINLLVPLRMPDKLEVQ-DDAVHGEERYAL 456
DB 400 VYTAVTFTVLKVLDMGLRVTBEEBAVGLDLALHNERGYNL 442

RESULT 5
H70310
ammonium transporter - Aquifex aeolicus
C/Species: Aquifex aeolicus
C/Date: 08-May-1998 #sequence_rev150n 08-May-1998 #text_change 09-Jul-2004
C/Accession: H70310
R/Beckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Oy

A/Cross-references: UNIPROT:O66515; UNIPARC:UPI000005627E; GB:AE000674; NID:92982850; PII
A/Experimental source: strain VF5
C/Genetics:
A/Gene: amtB
C/Superfamily: ammonium transporter nrgA

Query Match 27.9%; Score 706; DB 2; Length 423;
Best Local Similarity 35.7%; Pred. No. 1.4e-46;
Matches 157; Conservative 78; Mismatches 157; Indels 48; Gaps 9;

QY 24 LKKGDNAQVATVYGLQSVPGVLYGCVVKKKAAVNSAFMAVYAFAAWICWTMAY 83
DB 25 LDGTAMTALVAVSALVFTVTPGLALFYGLDLSKSIINTIAMSFSAPAVITLTFVVG 84
QY 84 NNSFGEKLPIWGKARPALDQGLLVGRALPATVHYRADGSVETAAVEPLYPATVYQ 143
DB 85 SVAYGDIQFEGIGN-----PFOVLKGGISGINSIDGYRPLDLMFO 126
QY 144 CVPAATTLIVVAGSLIGMSFLAMMIFVPLMTFSYTVGAFSIMGGGFLPHGVIDYCGG 203
DB 127 LTFATITTLISGSFVGRKFSAMILFALMSVFTVPPAAHVMWGGGFLANDGALDPAQ 186
QY 204 YVTHSAGIAGTAAVYVGPRAQKREPPNNILFTLGAQLMWMGAFNGGCPYAA 263
DB 187 TVVHINAGIAGVGLIIGRR--KDTSLI-PNNVPLVALGAGILWPGFPGFAGSALGAN 243
QY 264 SVASNAVLNTNICTAMSLIWTCLDVIFFKRSVGVCAVQGMITGLVCTTPAAGVQMAA 323
DB 244 ESAAMAMINTVYATSPALAMFTEMLHVGKPLVVGISGIVAGVATTPAAGFVNLGS 303
QY 324 LVWVAGSIPWTWMLIHKRSKILQRPVDTLGVPHHVGAGLLTGLFAEPTLCNL 383
DB 304 IFIGALIA-SVCAVFWALVKPK---FGYDLDLDFEIGHGVAGVAVLGVFAPDPAV--- 356
QY 384 FLPVADSRGAFYGGAGQFGK-----QIAGGLFVANNVYVTSLICLAINLVPLRN- 436
DB 357 -----GGTGLLGNPKQVLIQIEGVATITVSAITLAVITLVKAVGLRVS 404
QY 437 PDDKLEVGDVAHGEERYAL 456
DB 405 EEEIEELT-DSSLHGEKAYNL 423

RESULT 6
AF0381
probable ammonium transporter YPO3142 [imported] - Yersinia pestis (strain CO92)
C/Species: Yersinia pestis
C/Date: 02-Nov-2001 #sequence_rev150n 02-Nov-2001 #text_change 09-Jul-2004
C/Accession: AF0381
R/Fairchild, J.; Wren, B.W.; Thomson, N.R.; Tibball, R.W.; Holden, M.T.G.; Prentice, M.B.;
deno-Farraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
Hill, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Bartell, E
Nature 413, 523-527, 2001
A/Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A/Reference number: AB0001; NCID:21470413; PMID:11586360
A/Accession: AF0381
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-431 <EUR>
A/Cross-references: UNIPROT:Q8ZC80; UNIPARC:UPI000000DCE76; GB:AL590842; PIDN:CAC92377.1;
C/Genetics:
A/Gene: YPO3142
C/Superfamily: ammonium transporter nrgA

Query Match 27.3%; Score 691; DB 2; Length 431;
Best Local Similarity 35.3%; Pred. No. 2e-45;
Matches 157; Conservative 76; Mismatches 160; Indels 52; Gaps 9;

QY 19 SVADWINKDNAMQVLAATLVGLQSVPGVLYGCVVKKKAAVNSAFMAVYAFAAWICW 78
DB 28 AVAD--KADNAFMWICTALVLFMTIPGIALFYGLRSKIVLSMTQVWVSFALCVLM 84
QY 79 VTMAYNMSFGEKLLPIWGRA-RPALDQGLLVGRALPATVHYRADGSVETAAVEPLYPMA 137

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Dh      85  ILVGSIAFSFA-----GNAFFGSPDMAMLKG-----:ILTSLSGSEFYQ 123
Qy      138  TVVVFQCFEAFATITLILVAGSLGGRMSFLAMMI FVPLMLTFSYTVGAFSLGGCFLEFHWGV 197
Dh      124  IHVVFQASFACTIYALIVGSPAERIRFSAVILIFALMTTFYILPLAHVWGGGFLEANDGA 183
Qy      198  IDYCGGVYIHVSAGIAGCFATAAYVWVPPRAQKDREREPNNIIFTLTGAGLLMMWAGFNGG 257
Dh      184  LDFPGCGTVVHINAAVAGLVGAYLLGKRAGPQKRAKPHNLPMVFTGTILVIGNPGFRAG 243
Qy      258  GPVAAANSVASNAVINTNICTAMSLIWTCLDVIFFPKKPSVVGAVQGMITGLVCITTPAAGV 317
Dh      244  SASANAEIAPALAPLNTVATAGALISWFAEMALRGKSLGAGSGCIAGVAITTPAAGT 303
Qy      318  VQGNAAALVGVLAGSIPMYTMMILHKRSKILQKRDVDTLGVFHTHGACVLLGGLLTGFLAE 377
Dh      304  VGVGGALITIGLVGGAAGLVGLLKK-----MLRVDDTCDVGVGVGVCIVGICILTVGFTS 359
Qy      378  PTLNCLFLPVADSRGAFYGGAG---GAQFGQIAGGLF---VVAANNVYTSLICLAINTL 430
Dh      360  ASL-----GGTGTAAGVTMTHQGVQLFSVGVTVVWMSGVAVFVAFKIAGL 404
Qy      431  LVPLRMPDDKLEVGDDA-VHGSEAY 454
Dh      405  IVGLRVPEEQEREGLDVNSHGENAY 429

```

[illegible]

RESULT 7

AC0560
probable ammonium transporter amtb [imported] - Salmonella enterica subsp. enterica serovar typhimurium
C|Species: Salmonella enterica subsp. enterica serovar Typhi
A|Note: this species has also been called Salmonella typhi
C|Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C|Accession: AC0560

R|Parkhill, J., Dougan, G., James, K.D., Thomson, N.R., Pickard, D., Wain, J., Churcher, C., Tole, I., Connor, P., Cronin, A., Davis, P., Davies, R.M., Dowd, L., White, N., Farrar, S., M'Leary, S., O'Garra, P.
N|ature 413, 848-852, 2001

A|Authors: Parry, C.; Quail, M., Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.A.
A|Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serovar typhimurium
A|Reference number: AB0502; MUID:21534947; PMID:11677608

A|Accession: AC0560

A|Status: preliminary
A|Molecule type: DNA
A|Residues: 1-428 <PAR>
A|Cross-references: UNIPARC:UPI000005A206; GB:AL513382; PIDN:CAD08923.1; PID:g16501735; C|Genetics:

A|Gene: amtb
A|Superfamily: ammonium transporter nrgA

```

A:Molecule type: DNA
A:Residues: 1-433 <KUR>
A:Cross-references: UNIPROT:Q8UYB9, UNIPARC:UPI000005JB94, GB:AE008917, PIDN:AAL51349.1,
A:Experimental source: strain 16M
C:Genetics:
A:Gene: BMEI0167
A:Map position: I
C:Superfamily: ammonium transporter nrgA

Query Match      26.0%; Score 659; DB 2; Length 433;
Best Local Similarity 33.3%; Pred. No. 5,7e-43;
Matches 145; Conservative 80; Mismatches 168; Indels 42; Gaps 8;

QY      21  ADMLKKDPAQMDLVAAITVGLQSVPLVVLGYGVVKKKAAVNSAFMLYAPFAAVIMCVT  80
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db       34  APTLDTGTAAMLVSTALVDMMTIPGLALFYGGAMVKKNVLSTVMOSFAITCLMSILMMI  93

QY      81  WAYNMSF--GEKLLPIWGAAPALDQGLVGRALPATVYRADGSVETAAVBELPMAT  138
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db       94  AGYSIAFTDGGSLHSTYIGGFSKVFPSG--VTMESLGTI-----PEYL  134

QY     139  VVYFOCVFAAITLLVAGSLGRMSFLANMTIVPLMLTFSYTVGAFSLMGGFLFHWGVI  198

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	Query Match	26.0%	Score 660;	DB 2;	Length 428;	
	Best Local Similarity	35.8%	Pred. No. 4.8e-43;			
	Matches 159;	Conservative 73;	Mismatches 162;	Indels 50;	Gaps 10;	
OY	19 SVADMLNGDNAMQCLAAATLVLGLOSPEGLVYLGGVVKKKMAVNSAFMALYAFAAVWICM	78				
Db	25 AVAD---KADAPFMNICTALVLFMTIPGIALFYGLLIKAQVLSMLTGVYTFPFLVCILM	81				
OY	79 VTMAYNMSFGEKLPIWKGRARPALDQGLLVGBALPATVHYRADGSVEETAVERLYPMAT	138				
Db	82 VVYGSLAIFEGE-G-NHFFGNV-----DGAMLKNIAL-----TAVTGITTYQYIH	122				
OY	139 VVYPCCVPAALTLLIVAGSLLGRMSFLMMI FVPRLMTFSTYVGA.FSLMGGEFLHMCOVI	198				
Db	123 VA-FQSGPACTIVGLIVGALAEIRISAVLLFTVVVFETLSYIPAHMWGGGLLAARHAL	181				
OY	199 DYCGGYVIVHSAGINGFTAAYVWGSPRAOKDERFPENNILLFTLGAGLLMMGMAGFNQGG	258				
Db	182 DFAGTGTVHHINALINGLAVILIGRVRGCKEAFPHNLPMVFTGTALLTYIGMRPFNNQS	241				
OY	259 PPAANSVASMAVLNTNICTAMSLLVWTCLDVITFEKKPSVGVAQCMITGLVCTTPAACGV	318				

[illegible]

RESULT 9

ammonium transporter - Deinococcus radiodurans (strain R1)
B75487
C:Species: Deinococcus radiodurans
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: B75487
R:White, O.; Eissen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathavan, J.U.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
S: Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MUID:20036896; PMID:10567266
A:Accession: B75487
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-439 <MUI>
A:Cross-references: UNIPROT:Q9RWH5; UNIPARC:UPI0000003D23; GB:AE001926; GB:AE000513; NID
A:Experimental source: strain R1
C:Gene: DR0693
A:Map position: 1
C:Superfamily: ammonium transporter nrga

Query Match 25.9%; Score 655.5; DB 2; Length 439;
Best Local Similarity 33.0%; Pred. No. 1.3e-42;
Matches 153; Conservative 90; Mismatches 161; Indels 59; Gaps 12;

QY 2 SSATVPLAVYOGTASVAD---MLNKGNAMQVATVGLQSVPLVYGVVKKK 58
DB 12 TALLLLPL-----STFPAADAKHLDGTDTAMLMRALVPLMT-PGLAFPTGGLRAQ 66
QY 59 WAVNSAFMALYAFPAVMIQVTVAAVNSFSEKLLPIWKGKAPALDGLLVRAALPATVH 118
DB 67 SVLNTMMMSVSIIGLVGLVMTLAGYSIAFGD-----GCAWLGDPAH 107
QY 119 YRADSG-SVERAAVEPLYPMAITVYFQCVFPAITLILVAGSLDGRMSFLAMMIFVPLTLF 177
DB 108 LGNLGLAGLQGLTGTIPYVFAAS---FQAMPALIAVALISGAVEMRGAFILFPAALMTLI 164
QY 178 SYTVGAFSLMG-GGFLFMGVIVIDYCGGVVIVHSAGIAGFTAAVYVGRADKDERFPNN 236
DB 165 IYSPRLAMWVGANGKMLFKDGLADPAGGTIVHISGVALVAAMLLGRLGPRNAHPN 224
QY 237 ILFTLTGAGLLMGWAGFNGGPGPYAASVSAVAVLNTNICTAMSLIVTCLDVIFFKPS 296
DB 225 VPLVLGAGLLMGWGFNGFNGSALGANQTAALATITTLIAPAAMLTWLGESL-SSKPT 283
QY 297 VVGAVQMTITGLVCTITPAAGVQGMALVWGVLAGSIFPTTMMILHRSKILQVDTLG 356
DB 284 AVGAATGLVVGVAITPACAFVSFWAAVLLGILGATASVYTVQAKH-----LMAADALD 338
QY 357 VFHTHVGAGLLGGLTGLPAEPTCNLFPLVADSRGAFYGGAG---GAPFGKOIAGLFFV 413
DB 339 VFACHGAVGVGALLTGLLMTT-----GSGKPTAQNFTQLISVVAS 381
QY 414 VAMVVVTSICLAINILVPLRMBDDKLEVGDD-AVHGEEAAYA 455
DB 382 LTVAGVGSFLILKVLVPLRVPAAGEIAGIDLSAHQEGYS 424

RESULT 10

ammonium transporter amtb [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
H86823
C:Species: Lactococcus lactis subsp. lactis
C>Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
C:Accession: H86823
R:Boletoin, A.; Wincker, P.; Mauger, S.; Jallou, O.; Malarme, K.; Weisenbach, J.; Ehrlich
Genome Res. 11, 731-753, 2001
A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s
A:Reference number: A86625; MUID:21235186; PMID:11337471
A:Accession: H86823
A:Status: preliminary

A:Molecule type: DNA
A:Residues: 1-413 <STO>
A:Cross-references: UNIPROT:Q9CF89; UNIPARC:UPI000000CGA8D; GB:AE005176; PTD:912724597; P
A:Experimental source: strain IL1403
C:Gene: amtb
C:Superfamily: ammonium transporter nrga

Query Match 25.7%; Score 652; DB 2; Length 413;
Best Local Similarity 34.0%; Pred. No. 1.9e-42;
Matches 150; Conservative 72; Mismatches 173; Indels 46; Gaps 9;

QY 24 LNKGNAMQVATVGLQSVPLVYGVVKKKAVNSAFMALYAFPAVMIQVTVAAV 83
DB 1 MDGSIAPILICAAVPLMT-PALAFPTGGLGRKRVLTMMSLAPMALASTLMIIGF 59
QY 84 NMSFGKLLPIWKGKAPALDGLLVRAALPATVHYRADSGVETAAVEPLYPMATV---- 139
DB 60 SFSFS-----GSNGWIGDFHILFMNGVDMAK-NSLFPANHIPDGL 98
QY 140 -VTFQCVFPAITLILVAGSLDGRMSFLAMMIFVPLTSTYVAGASLNGGFLFMGV 198
DB 99 FSGFQMMFSITVPLITGSGVGRMRPTPLIFMTAWLILVYPLAMVWGGGLAQIHA 158
QY 199 DYCGGVIVHSAGIAGFTAAVYVGRADKDERFPNNILFTLTGAGLLMGWAGFNGG 258
DB 159 DFAGSDVHISGVTGLGLVIGKRDYRDLRPHNIPFVLGAGLLMGWGFNGS 218
QY 259 PYAANSVSAVAVLNTNICTAMSLIVTCLDVIFFKPSVVGAVQMTITGLVCTITPAAGV 318
DB 219 ALANGAVAIAPFTTTAAVAAAMFMSWIVYEKILIGRPSIVGASGAVGLVATPGAGV 278
QY 319 QGNAAVWGVLAGSIFPTTMMILHRSKILQVDTLGVPHTHVGAGLLGGLTGLPAEP 378
DB 279 SLWSSILIGLVPLSYFMISVYKKK---LGSDALDAPFGCGIGMFGMTGIFATP 334
QY 379 TLGNLPLVADSRGAFYGGAGGAPFGKOIAGLFFVAMVVVTSL-----ICLAINILVPL 434
DB 335 ALA-----PEKGVGLIYG-----GKLLANVASVVFVIFALVSMIIKIALFMP 384
QY 435 RMPDDKLEVG-DDAVHGEAAY 454
DB 385 RVSDRAAIAIGLDSSBHEETAY 405

RESULT 11

ammonium transporter CC1338 [imported] - Caulobacter crescentus
C87415
C:Species: Caulobacter crescentus
C>Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C:Accession: C87415
R:Nierman, W.C.; Feldblum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eissen, J.; Heidelberg, J.I
B.; Laub, M.T.; Deboy, R.T.; Dodson, R.J.; Durkin, A.S.; Gilm, M.L.; Haft, D.H.; Kolom
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of Caulobacter crescentus.
A:Reference number: A87249; MUID:21173698; PMID:11255647
A:Accession: C87415
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-510 <STO>
A:Cross-references: UNIPROT:Q9A8U5; UNIPARC:UPI000000C735A; GB:AE005673; NID:913422685; P
C:Gene: CC1338
C:Superfamily: ammonium transporter nrga

Query Match 25.7%; Score 651.5; DB 2; Length 510;
Best Local Similarity 32.3%; Pred. No. 2.3e-42;
Matches 159; Conservative 78; Mismatches 179; Indels 77; Gaps 11;

QY 3 SSATVPLAVYOGTASVADMLNKGNAMQVATVGLQSVPLVYGVVKKKAVN 62
DB 52 ABAAPAPAA-----APTIEDKMDKGNAMMLTJALLVLMILPGLALFPGGLVRAK-NML 105


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Db       122 HVA-FQGSFACITVGLIGALAEIRFSAVLIFVVWMLTSLYPIAHMWGGGILLASHGA 180
Oy       198 IDYCGGYIVHVSAGIAGTTAAVVGPPRAOKDEREPENNILFTLTGAGLLMMMGAFNGG 257
Db       181 LDFPGAGTVVHHNAALAGLVGAYLLIKRFVGFGEAKRPNHLPMVFGTALTALLYGMFEFPNAG 240
Oy       258 GPYAANSVASMAVLNTMNLCTMSLIWTCCLDVIFPKKPSVSGAVOQMIGTLVCITPAAGV 317
Db       241 SAGTNNEIALALFVNVTVAATAAATLIGMTFGEMALAKGPBLLGRCSAIGLVGVTPACGY 300
Oy       318 VQGWAALVMGVLAGSIPMYTMMLHKRSKIQRVDDTLGVPHTHGAGLLGLLTGLFAE 377
Db       301 IGVGALLIIIVAGLAGLMGVMTL---KRLLRVDDPCDVFEGHVGCIVGCIIMTGIFA 356
Oy       378 PTLCTFLFPVADSRCAFPGAG---GAOPRGKIAGL----FVAMNVVVTSLICLAInL 450
Db       357 SSL-----GGVFGABGVTHGHQLVLQBSIAITTWMSGVAFIGYKLADL 401
Oy       431 LVPLMPDDKLEVGDA-VHGEAY 454
Db       402 TVGLRVPEEREGRLDVNSHENAY 426

RESULT 15
A90692
probable ammonium transporter ECo505 [imported] - Escherichia coli (strain O157:H7, subse
C.Species: Escherichia coli
C.Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C.Accession: A90692
R.Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.;
Gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A.Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genom
A.Reference number: A96629; MUID:21156231; PMID:11258796
A.Accession: A90692
A.Status: Preliminary
A.Molecule type: DNA
A.Residues: 1-428 <HAY>
A.Cross-references: UNIPROT:P37905; UNIPARC:UP10000125A44; GB:BA000007; PIDN:BA833928.1;
A.Experimental source: strain O157:H7, substrain RIMD 0509952
C.Genetic8:
A:Gene: ECo505
C:Superfamily: ammonium transporter nrgA

Query Match      25.7%; Score 650; DB 2; Length 428;
Best Local Similarity 34.6%; Pred. No. 2.8e-42;
Matches 154; Conservative 77; Mismatches 162; Indels 52; Gaps 10;

Oy       19 SVADLNKGDNAMQVLAATLVGLQSVPGLVVLVYGCVKKKMAVNSAFMALYAFAAVICW 78
Db       25 AVAD---KADNAPFMWICTALVLFMTIPGIALFYGGILRGKVLSMLTYVTFFALCILW 81
Oy       79 VTWAYNMSFGEKRLPIWGKARPALDOGLVGPAAIPATVHYRADSGVE-TAAVEPLYPMA 137
Db       82 VVYGSIASLAFGR-----GNMF- GNINWMMLKNIEPTAWGSIYOYT 121
Oy       138 TVVYQCCEFAATTLLVAGSLGRMSFLAMI.FVPLMTFSYTVGASFSLMGCGFLPFHMV 197
Db       122 HVA-FQGSFACITVGLIGALAEIRFSAVLIFVVWMLTSLYPIAHMWGGGILLASHGA 180
Oy       198 IDYCGGYIVHVSAGIAGTTAAVVGPPRAOKDEREPENNILFTLTGAGLLMMMGAFNGG 257
Db       181 LDFPGAGTVVHHNAALAGLVGAYLLIKRFVGFGEAKRPNHLPMVFGTALTALLYGMFEFNAG 240
Oy       258 GPYAANSVASMAVLNTMNLCTMSLIWTCCLDVIFPKKPSVSGAVOQMIGTLVCITPAAGV 317
Db       241 SAGTNNEIALALFVNVTVAATAAATLIGMTFGEMALRGKPBLLGRCSAIGLVGVTPACGY 300
Oy       318 VQGWAALVMGVLAGSIPMYTMMLHKRSKIQRVDDTLGVPHTHGAGLLGLLTGLFAE 377
Db       301 IGVGALLIIIVAGLAGLMGVMTL---KRLLRVDDPCDVFEGHVGCIVGCIIMTGIFA 356
Oy       378 PTLCTFLFPVADSRCAFPGAG---GAOPRGKIAGL----FVAMNVVVTSLICLAInL 450
Db       357 SSL-----GGVFGABGVTHGHQLVLQBSIAITTWMSGVAFIGYKLADL 401
Oy       431 LVPLMPDDKLEVGDA-VHGEAY 454
Db       402 TVGLRVPEEREGRLDVNSHENAY 426

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OY	378	PTLCNLFLEPVADSRGAFYCGAG---	GAORQOIAGL----	FVAMNVVYTSLICIAINTL	430
Db	357	SSL-----	-GGVGFAEGVTNGHQLVQLESIAITTVMSGVAFIGYKLADL		401
OY	431	LVPLRMPDDKLEVDDA-VHGEAY			454
Db	402	TVGLRVPEEQEREGLDVNSHENAY			426

Search completed: July 22, 2006, 03:33:42
Job time : 42 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: July 22, 2006, 03:34:51 ; Search time 29 Seconds
(Without alignments)
952,519 Million cell updates/sec

Title: US-10-713-648A-63
Perfect score: 2534
Sequence: 1 MSSSATVPLAYOGNTSASV.....GEMVDTKKGSDAAVAPVV 479

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 208217 seqs, 57668156 residues

Total number of hits satisfying chosen parameters: 208217

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Published Applications AA.New.*
1: /EMC_Celerra_SIDS3/prodata/1/pubpaa/US09_NEW_PUB pep.*
2: /EMC_Celerra_SIDS3/prodata/1/pubpaa/US06_NEW_PUB pep.*
3: /EMC_Celerra_SIDS3/prodata/1/pubpaa/US07_NEW_PUB pep.*
4: /EMC_Celerra_SIDS3/prodata/1/pubpaa/US08_NEW_PUB pep.*
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7: /EMC_Celerra_SIDS3/prodata/1/pubpaa/US11_NEW_PUB pep.*
8: /EMC_Celerra_SIDS3/prodata/1/pubpaa/US60_NEW_PUB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2534	100.0	479	US-10-713-648A-63	Sequence 63, Appl
2	2527	99.7	479	US-10-449-902-5313	Sequence 5313, A
3	1931	76.2	369	US-10-449-902-47331	Sequence 47331, A
4	1714	67.6	486	US-10-449-902-43179	Sequence 43179, A
5	1693.5	66.8	497	US-10-449-902-35281	Sequence 35281, A
6	1682.5	66.4	475	US-10-953-349-10298	Sequence 10298, A
7	1647	65.0	419	US-10-449-902-39814	Sequence 39814, A
8	1569.5	61.9	440	US-10-953-349-10299	Sequence 10299, A
9	1472.5	58.1	418	US-10-953-349-10300	Sequence 10300, A
10	1003.5	39.6	255	US-10-953-349-17239	Sequence 17239, A
11	951	37.5	304	US-10-449-902-54997	Sequence 54997, A
12	881	34.8	218	US-10-953-349-17240	Sequence 17240, A
13	845	33.3	208	US-10-953-349-17241	Sequence 17241, A
14	769	30.3	219	US-10-449-902-40126	Sequence 40126, A
15	589	23.2	428	US-10-471-571A-244	Sequence 244, App
16	547	21.6	486	US-11-185-301-2	Sequence 2, Appl1
17	530	20.9	524	US-10-449-902-49921	Sequence 49921, A
18	474.5	18.7	492	US-11-251-208-73	Sequence 24, Appl
19	344.5	13.6	507	US-11-296-657-24	Sequence 24, Appl
20	343.5	13.6	518	US-11-296-657-25	Sequence 25, Appl
21	337.5	13.3	514	US-11-296-657-23	Sequence 23, Appl
22	329	13.0	496	US-11-296-657-26	Sequence 26, Appl
23	327.5	12.9	513	US-11-296-657-27	Sequence 27, Appl
24	326	12.9	514	US-11-296-657-32	Sequence 22, Appl
25	325.5	12.8	519	US-11-296-657-33	Sequence 33, Appl

26	323	12.7	496	US-10-449-902-38313	Sequence 38313, A
27	313.5	12.4	500	US-11-251-208-447	Sequence 447, Appl
28	305	12.0	484	US-11-296-657-32	Sequence 32, Appl
29	301	11.9	488	US-11-296-657-30	Sequence 30, Appl
30	297	11.7	498	US-11-296-657-34	Sequence 34, Appl
31	291.5	11.5	488	US-10-449-902-51990	Sequence 51990, A
32	291.5	11.5	488	US-11-296-657-31	Sequence 31, Appl
33	291.5	11.5	532	US-11-296-657-28	Sequence 28, Appl
34	291.5	11.5	532	US-11-296-657-29	Sequence 29, Appl
35	276.5	10.9	492	US-10-449-902-36776	Sequence 36776, A
36	115.5	4.6	189	US-10-992-149-11	Sequence 11, Appl
37	111.5	4.4	500	US-10-449-902-28844	Sequence 28844, A
38	111.5	4.4	643	US-10-471-571A-4394	Sequence 4394, Ap
39	109	4.3	656	US-10-449-902-45299	Sequence 45299, A
40	103.5	4.1	443	US-11-056-3558-18881	Sequence 18881, A
41	103.5	4.1	487	US-11-056-3558-18880	Sequence 18880, A
42	102.5	4.1	955	US-10-449-902-41322	Sequence 41322, A
43	102.5	4.0	427	US-11-056-3558-18882	Sequence 18882, A
44	102.5	4.0	459	US-10-471-571A-472	Sequence 472, Appl
45	102.5	4.0	1052	US-10-497-088-21	Sequence 21, Appl

ALIGNMENTS

RESULT 1
US-10-713-648A-63
; Sequence 63, Application US/10713648A
; Publication No. US20060107344A1
; GENERAL INFORMATION:
; APPLICANT: POSCO
; APPLICANT: POSTECH
; APPLICANT: An, Gynheung
; APPLICANT: Ryu, Choong-Hwan
; APPLICANT: Han, Jong-Jin
; APPLICANT: Kang, Hong-Gyu
; APPLICANT: An, Kyungsok
; TITLE OF INVENTION: ORGAN PREFERENTIAL GENES IDENTIFIED BY T-DNA INSERTIONAL
; FILE REFERENCE: 20010-04USA
; CURRENT APPLICATION NUMBER: US/10/713,648A
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/427,166
; PRIOR FILING DATE: 2002-11-15
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 63
; LENGTH: 479
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURES:
; NAME/KEY: PEPTIDE
; LOCATION: (0)..(0)
; OTHER INFORMATION: line 1C-109-35 polypeptide sequence
US-10-713-648A-63
Query Match 100.0%; Score 2534; DB 6; Length 479;
Best Local Similarity 100.0%; Pred. No. 2.1e-198;
Matches 479; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSSSATVPLAYOGNTSASVADMLNKGDNAWQVLAATLVGLQSVPLGVLYXGVVKKKWA 60
Db 1 MSSSATVPLAYOGNTSASVADMLNKGDNAWQVLAATLVGLQSVPLGVLYXGVVKKKWA 60
QY 61 VNSAFMALVFAFAVWICMTWAVYMSFGKELLPWGRKARPALDOGLVGRAPALPATVHYR 120
Db 61 VNSAFMALVFAFAVWICMTWAVYMSFGKELLPWGRKARPALDOGLVGRAPALPATVHYR 120
QY 121 ADGSGVETAAVEPLYPNATVYVFOCVPAATLILVAGSLGRMSFLAMITVPLMLTFSYT 180
Db 121 ADGSGVETAAVEPLYPNATVYVFOCVPAATLILVAGSLGRMSFLAMITVPLMLTFSYT 180
QY 181 VGNFSLMGSGFLFRHWGVIDVCGGVVHVSAGIAGFTAAVWVGPRAQDRRFPNNILFT 240

Db 181 VGAFSLMGGGFLFHHGVIDYCGGYVHVSAGIAGFTAAVWGPRADKDERPPNNILFT 240
Qy 241 LTGAGLLMGMAGFNGGGGYAANSVASMALVNTNICTAMSLIYWTCLDVIFFKKSUVGA 300
Db 241 LTGAGLLMGMAGFNGGGGYAANSVASMALVNTNICTAMSLIYWTCLDVIFFKKSUVGA 300
Qy 301 VCGMITGLVCITPAAGVVGMAALVWGVLAGSIPWYTMILHKRSKIILORVDDTLGVFHT 360
Db 301 VCGMITGLVCITPAAGVVGMAALVWGVLAGSIPWYTMILHKRSKIILORVDDTLGVFHT 360
Qy 361 HGVAGLLGGLLTGLFAEPTLCNLFLPVADSRGAFYGGAGAGQFGKQIAGGLFVVAAMNVV 420
Db 361 HGVAGLLGGLLTGLFAEPTLCNLFLPVADSRGAFYGGAGAGQFGKQIAGGLFVVAAMNVV 420
Qy 421 TSLICLAINLVPLRMPDDKLEVGDDAVHGEBAVALMGDEMYDVTYKGSDAVAAPVVV 479
Db 421 TSLICLAINLVPLRMPDDKLEVGDDAVHGEBAVALMGDEMYDVTYKGSDAVAAPVVV 479

RESULT 2
US-10-449-902-53313

/ Sequence 53313, Application US/10449902
/ Publication No. US20060123505A1
/ GENERAL INFORMATION:
/ APPLICANT: National Institute of Agricultural Sciences.
/ APPLICANT: Bio-oriented Technology Research Advancement Institution.
/ APPLICANT: The Institute of Physical and Chemical Research.
/ APPLICANT: Foundation for Advancement of International Science.
/ TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
/ FILE REFERENCE: MOA-A0205Y1-US
/ CURRENT APPLICATION NUMBER: US/10/449,902
/ CURRENT FILING DATE: 2003-05-29
/ PRIOR APPLICATION NUMBER: JP 2002-203269
/ PRIOR FILING DATE: 2002-05-30
/ PRIOR APPLICATION NUMBER: JP 2002-383870
/ PRIOR FILING DATE: 2002-12-11
/ NUMBER OF SEQ ID NOS: 56791
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 53313
/ LENGTH: 479
/ TYPE: PRF
/ ORGANISM: Oryza sativa
/ US-10-449-902-53313

Query Match 99.7%; Score 2527; DB 6; Length 479;
Best Local Similarity 99.6%; Pred. No. 7.7e-198;

Matches 477; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSSSATVVEFLAYQNTSASVADMLNKGDANMOLVAATLVGLOSVPGLVVLGGVVKKKMA 60
Db 1 MSSSATVVEFLAYQNTSASVADMLNKGDANMOLVAATLVGLOSVPGLVVLGGVVKKKMA 60
Qy 61 VNSAFNALYAFAAWVICWTWYNNMSFGEKLPIMWKARPALDOGLLVRAALPATVHR 120
Db 61 VNSAFNALYAFAAWVICWTWYNNMSFGEKLPIMWKARPALDOGLLVRAALPATVHR 120
Qy 121 AGGSVETAVERPIYPAATVYVFOCVPAATLLIVASSLLGRMSFLAMIFVPLMLTFSTT 180
Db 121 AGGSVETAVERPIYPAATVYVFOCVPAATLLIVASSLLGRMSFLAMIFVPLMLTFSTT 180
Qy 181 VGAFSLMGGGFLFHHGVIDYCGGYVHVSAGIAGFTAAVWGPRADKDERPPNNILFT 240
Db 181 VGAFSLMGGGFLFHHGVIDYCGGYVHVSAGIAGFTAAVWGPRADKDERPPNNILFT 240
Qy 241 LTGAGLLMGMAGFNGGGGYAANSVASMALVNTNICTAMSLIYWTCLDVIFFKKSUVGA 300
Db 241 LTGAGLLMGMAGFNGGGGYAANSVASMALVNTNICTAMSLIYWTCLDVIFFKKSUVGA 300
Qy 301 VCGMITGLVCITPAAGVVGMAALVWGVLAGSIPWYTMILHKRSKIILORVDDTLGVFHT 360
Db 301 VCGMITGLVCITPAAGVVGMAALVWGVLAGSIPWYTMILHKRSKIILORVDDTLGVFHT 360

Qy 361 HGVAGLLGGLLTGLFAEPTLCNLFLPVADSRGAFYGGAGAGQFGKQIAGGLFVVAAMNVV 420
Db 361 HGVAGLLGGLLTGLFAEPTLCNLFLPVADSRGAFYGGAGAGQFGKQIAGGLFVVAAMNVV 420
Qy 421 TSLICLAINLVPLRMPDDKLEVGDDAVHGEBAVALMGDEMYDVTYKGSDAVAAPVVV 479
Db 421 TSLICLAINLVPLRMPDDKLEVGDDAVHGEBAVALMGDEMYDVTYKGSDAVAAPVVV 479

RESULT 3
US-10-449-902-47331

/ Sequence 47331, Application US/10449902
/ Publication No. US20060123505A1
/ GENERAL INFORMATION:
/ APPLICANT: National Institute of Agricultural Sciences.
/ APPLICANT: Bio-oriented Technology Research Advancement Institution.
/ APPLICANT: The Institute of Physical and Chemical Research.
/ APPLICANT: Foundation for Advancement of International Science.
/ TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
/ FILE REFERENCE: MOA-A0205Y1-US
/ CURRENT APPLICATION NUMBER: US/10/449,902
/ CURRENT FILING DATE: 2003-05-29
/ PRIOR APPLICATION NUMBER: JP 2002-203269
/ PRIOR FILING DATE: 2002-05-30
/ PRIOR APPLICATION NUMBER: JP 2002-383870
/ PRIOR FILING DATE: 2002-12-11
/ NUMBER OF SEQ ID NOS: 56791
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 47331
/ LENGTH: 369
/ TYPE: PRF
/ ORGANISM: Oryza sativa
/ US-10-449-902-47331

Query Match 76.2%; Score 1931; DB 6; Length 369;
Best Local Similarity 99.7%; Pred. No. 1.6e-149;

Matches 364; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 115 ATVHYRADGSVETAVERPIYPAATVYVFOCVPAATLLIVAGSLGRMSFLAMIFVPLM 174
Db 5 ATVHYRADGSVETAVERPIYPAATVYVFOCVPAATLLIVAGSLGRMSFLAMIFVPLM 64
Qy 175 LTFSTYVGAFLMGGGFLFHHGVIDYCGGYVHVSAGIAGFTAAVWGPRADKDERPP 234
Db 65 LTFSTYVGAFLMGGGFLFHHGVIDYCGGYVHVSAGIAGFTAAVWGPRADKDERPP 124
Qy 235 NNILFTLTCAGLLMGMAGFNGGGGYAANSVASMALVNTNICTAMSLIYWTCLDVIFFK 294
Db 125 NNILFTLTCAGLLMGMAGFNGGGGYAANSVASMALVNTNICTAMSLIYWTCLDVIFFK 184
Qy 295 PSVGAVOGMTGLVCITPAAGVVGMAALVWGVLAGSIPWYTMILHKRSKIILORVDDT 354
Db 185 PSVGAVOGMTGLVCITPAAGVVGMAALVWGVLAGSIPWYTMILHKRSKIILORVDDT 244
Qy 355 LCVFTHGVAGLLGGLLTGLFAEPTLCNLFLPVADSRGAFYGGAGAGQFGKQIAGGLFV 414
Db 245 LCVFTHGVAGLLGGLLTGLFAEPTLCNLFLPVADSRGAFYGGAGAGQFGKQIAGGLFV 304
Qy 415 ANNVAVTSICLAINLVPLRMPDDKLEVGDDAVHGEBAVALMGDEMYDVTYKGSDAV 474
Db 305 ANNVAVTSICLAINLVPLRMPDDKLEVGDDAVHGEBAVALMGDEMYDVTYKGSDAV 364
Qy 475 APVVV 479
Db 365 APVVV 369

RESULT 4
US-10-449-902-43179

/ Sequence 43179, Application US/10449902
/ Publication No. US20060123505A1
/ GENERAL INFORMATION:
/ APPLICANT: National Institute of Agricultural Sciences.

APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 43179
LENGTH: 486
TYPE: PR1
ORGANISM: Oryza sativa
US-10-449-902-43179

Query Match 67.6%; Score 1714; DB 6; Length 486;
Best Local Similarity 69.0%; Pred. No. 9.1e-132;
Matches 319; Conservative 51; Mismatches 82; Indels 10; Gaps 4;

10 LAYQNTSAS--VADMLNKGNAMOLVAATLVGLQSVGLVYGVVKKKMAVNSAFM 66
1 MAAAGAYSASLPVPDLNKGNAMOLTAATLVGLQSMPLVLYGSIVKKMAVNSAFM 60
67 ALYAFAMVICWVTMAVYNSFGEKLLPIWGKARPALDQGLLVGRAALPATVHYRADGSVE 126
61 ALAYASSLVWVTVGFBRAGFDQLLPFGKAGVALLQSVLVGRATLPATRAH----GAL- 115
127 TAAVEFLPMATVYVYQCFFPAATLTLLVAGSLGRMSFLAMMIFVPLMLTFSTYVGAFL 186
116 -PRTEPFYEPATLVLPQFEPAITLVLAGSVIGRMNIKAMAFPLMLLSYVGAFLSL 174
187 MGGGFPHNGVIDYCGGYVYHVSAGIAGFAAYVWVGPRADKREPPNNILFTLGAGL 246
175 MGGGFYRKGVIDYSGGYVYHLSGGIAGFAAYVWVGPRADKREPPNNILMTAGGL 234
247 LWMGAGFNGGGRFYAANSVAMAVLNTNI CTAMSLVWTCLDVIFPKKPSVGAVOGMT 306
235 LWMGAGFNGGGRFYAANSVAMAVLNTNVCATSLMTCLDVIFPKKPSVGAVOGMT 294
307 GLVCIIPAAAGVVGAAALVWGLAGSI PWTMMILHKSKILLORVDDTLGVFHTHGAFL 366
295 GLVCITPGAGLVGTMAAVVMGIFAGSVPMFTMMILHKSKALLMKKVDTLAVFHTHVAAGL 354
367 LGGLLGLFAEPTLCULFVADSRAFGVGAAGAGFGKQIAGGLFVAMNVVTSILCL 426
355 LGGILGLLATPPLFSLSESTVPGLRGAFYGG-GIKQIGKQAGAAFYIANNLVTTAILL 413
427 AINLVLPRMPDLEKLEVDVAHGEAYALMGDEMYDVTKH 468
414 GIGLFIPLMRPDQIMIGDPAAHGEAYALMGDEKFDATRH 455

RESULT 5
US-10-449-902-35281
Sequence 35281, Application US/10449902
Publication No. US20060123505A1
GENERAL INFORMATION:
APPLICANT: National Institute of Agricultural Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR FILING DATE: 2002-12-11

NUMBER OF SEQ ID NOS: 56791
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 35281
LENGTH: 497
TYPE: PR1
ORGANISM: Oryza sativa
US-10-449-902-35281

Query Match 66.8%; Score 1693.5; DB 6; Length 497;
Best Local Similarity 67.9%; Pred. No. 4.3e-130;
Matches 305; Conservative 54; Mismatches 89; Indels 1; Gaps 1;

19 SVADMLNKGNAMOLVAATLVGLQSVGLVYGVVKKKMAVNSAFMALYAPAAWICM 78
16 AVPAMLNKGDITAMQALTAATLVGLQSMPLVLYGSIVKKMAVNSAFMALYASTLIW 75
79 VTMAVNSFGEKLLPIWGKARPALDQGLLVGRAALPATVHYRADGSVEETAPEPLPMAT 138
76 VLVGFBRAGDRLPFWAKAGPALTDQFLVQAVFPATAHYSDGTLETPTPEFYAEMA 135
139 VYFQCVPAAITLTVAGSLGRMSFLAMMIFVPLMLTFSTYVGAFLMGGGFLFMGYI 198
136 LVLFEEFEPAITLVLAGSLGRMNKAMMAFTPLMLFSYVVGAFSLMGGFLYQMGVI 195
199 DYCGGVYHVSAGIAGFAAYVWVGPRADKREPPNNILFTLGAGLLMAGFNGGA 258
196 DYSGGVYHLSGVAFPTAAYVWVGPRADKREPPNNILMTAGGLMTAGFNGGA 255
259 PYAANSVAMAVLNTNI CTAMSLVWTCLDVIFPKKPSVGAVOGMTGLVCITPAAGV 318
256 PYAPNTATVAVLNTNVSATSLTWTCLDVIFPKKPSVGAVOGMTGLVCITPAAGV 315
319 QGMAALVWGLAGSIWYTMILHKSKILLORVDDTLGVFHTHGAAGLGLTGFAPR 378
316 HTWSAMLMGMFAGSVPMFTMMILHKSKITLMKVDTLAVFHTHVAAGLGLVTLGFAPR 375
379 TFCNLFVADSRAFGVGAAGAGFGKQIAGGLFVAMNVVTSILCLAINLVLPRMPD 438
376 ELICALDCPLPNNRGVY-SSGIGQLKQGLGALFVYVMDLVTSAILLCLGFIPLMRBD 434
439 DKLEVDVAHGEAYALMGDEMYDVTK 467
435 DQIMIGDPAAHGEAYALMGDEKFDVTR 463

RESULT 6
US-10-953-349-10298
Sequence 10298, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nikolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 10298
LENGTH: 475
TYPE: PR1
ORGANISM: Arabidopsis thaliana
US-10-953-349-10298

Query Match 66.4%; Score 1682.5; DB 6; Length 475;
Best Local Similarity 66.8%; Pred. No. 3.2e-129;
Matches 300; Conservative 61; Mismatches 77; Indels 11; Gaps 1;

20 VADMLNKGNAMOLVAATLVGLQSVGLVYGVVKKKMAVNSAFMALYAPAAWICM 79
12 VPEMLNKGNAMOLTAATLVGLQSMPLVLYGSIVKKMAVNSAFMALYAPAAWICM 71
80 TMAVNSFGEKLLPIWGKARPALDQGLLVGRAALPATVHYRADGSVEETAPEPLPMATV 139

Db 72 LCTYMARBEELLPFPGKGGPAFDGQVYLKGAQKIP-----NSNVAPYFPMATL 120
QY 140 VYFOCVPAITLTLVAGSLGRMSFLAMNI FVPLMTFSYTVGASLWGGGLFPHKGVID 199
Db 121 VYFOCTFAITTLVAGSVLGRMNIAKAMNA FVPLMLIFSYTVGANSIMWGGGLYQWGVID 180
QY 200 YGGGVYIHVSAGIAGTAAYVWGPRAQXDRERPPNNILFTLTGAGLLMGMAGFPGGGR 259
Db 181 YSGGVYIHSSVAGFVAAYWGPRAKDRERPPNNVLLMAGGLMGMAGSGRNGGAP 240
QY 260 YAANSVASMAYLNTNICTAMSLIWTCLDVIFFKKPSVVGAVQGMITGVCITPAAGVQ 319
Db 241 YAANLTSSIAVANTNLMSATSLIWTTLTDLVIFFGKPSVIGALQGMVGTAGVTPGAGLIQ 300
QY 320 GMAALVWGLASIPYTMTHLHKSKILQKRVDDTLGVHTHGVAGLLGGLLTGFAERT 379
Db 301 TMAAIIIGVSGTAPVASMNIHKKSALQKVDTLAVFYTHAVAGLLGIMTGLFAHBD 360
QY 380 LCNLFPLVADSRGAFYGGAGAGQFGKQIAGL FVYAMNVVTSILCLAINLVLPLRMPD 439
Db 361 LCVLVLPLPATRGAFYGGAGKQKQLKQAGAAFIYAMNVVSTIILAIRVFIPLRMAE 420
QY 440 KLEVGDDAVHGEBAVALWMDGEMVDTYTKH 468
Db 421 ELGIGDDAHGEEAVALWMDGEEKFDATRH 449

RESULT 7
US-10-449-902-39814
; Sequence 39814, Application US/10449902
; Publication No. US20060123505A1

; GENERAL INFORMATION:
; APPLICANT: National Institute of Agricultural Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 39814
; LENGTH: 419
; TYPE: PRT
; ORGANISM: *Oryza sativa*
US-10-449-902-39814

Query Match 65.0%; Score 1647; DB 6; Length 419;
Best Local Similarity 72.2%; Pred. No. 2, 2e-126;
Matches 291; Conservative 52; Mismatches 60; Indels 0; Gaps 0;

QY 66 MALVFAANWICWMAVYMSFGKLLPWTGKARPLDGLLVGRALPATYHYRADGV 125
Db 1 MALVFAAAMWICWMAVYMSFGDRLPFGKARPLQSGFLVAQSELTAIRYHNSGA 60
QY 126 ETTAAVEPLVPMATVYFOCVPAITLTLVAGSLGRMSFLAMNIFVPLMTFSYTVGAS 185
Db 61 EAPMLKPLVPAITVYFOCVPMASITIIILAGSLGRMNIAKAMNAFVPLMTFSYTVGAS 120
QY 186 LMGGGLFPHWGVIDYCGGVYIHVSAGIAGTAAYVWGPRAQXDRERPPNNILFTLTGAG 245
Db 121 LMGGGLFQWGVIDYSGGVYIHSSGIAGLTAAYWGPASASDRERPPNNILVLVLAG 180
QY 246 LLMGMAGNGGFPYAANSVASMAYLNTNICTAMSLIWTCLDVIFFKKPSVVGAVQGM 305
Db 181 LLMGMAGNGGFPYASANIDSSMAVYLNTHICASTSLVTTIILDVFFGKPSVIGAVQGM 240

QY 306 TGLVCTPAGVYQGMALVWGLAGSIPTMTMTHHKSKILORVDDTLGVHTHGVAG 365
Db 241 TGLVCTTGAAGLVQGMALVWGLAGSIPTMTMTHHKSKSEMDIDTLGVHTHAGV 300
QY 366 LIGGLLTGLFAPPTLCNLFPLVADSRGAFYGGAGAGQFGKQIAGL FVYAMNVVTSILIC 425
Db 301 FLGAGATGLFAPPTLCNLFPLSIPDSKAFYGGAGSGQFGKQIAGL FVYAMNVVTSITC 360
QY 426 LAIINLPLRMPDDTLGVHTHGVAGLLGGLLTGFAERT 468
Db 361 VIISLILPLRIADDELIGDDAVHGEBAVALWMDGELNDMTH 403

RESULT 8
US-10-953-349-10299
; Sequence 10299, Application US/10953349
; Publication No. US20060107345A1

; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 10299
; LENGTH: 440
; TYPE: PRT
; ORGANISM: *Arabidopsis thaliana*
US-10-953-349-10299

Query Match 61.9%; Score 1569.5; DB 6; Length 440;
Best Local Similarity 65.6%; Pred. No. 4, 5e-120;
Matches 279; Conservative 60; Mismatches 75; Indels 11; Gaps 1;

QY 44 VGLVVLVGVWKKKMAVNSAFMALYAFPAAMWICWMAVYMSFGKLLPWTGKARPLD 103
Db 1 MGVILVLAIVKMKMAVNSAFMALYAFPAALVLCVLLCYMARBEELLPFMGKGGPAFD 60
QY 104 OGLVGRALPATYHYRADGSVETRAVEPLYPMATVYFOCVPAITLTLVAGSLGRMS 163
Db 61 OGYLKGAKIP-----NSNVAPYFPMATLVYFOCTFAITTLVAGSVLGHMN 109
QY 164 FLAMNIFVPLMTFSYTVGAFSLWGGGLFPHKGVIDYCGGVYIHVSAGIAGTAAYVGP 223
Db 110 IKAMNAFVPLMTFSYTVGAFSLWGGGLFYQMGVIDISGGVYIHSSVAGFVAAYWGP 169
QY 224 RAQXDRERPPNNILFTLTGAGLLMGMAGNGGFPYAANSVASMAYLNTNICTAMSLIV 283
Db 170 RPKADRERPPNNVLLMAGGLMGMAGSGRNGGAPYANLTSSIAVANTNLMSATSLIV 229
QY 284 WTCLDVIFFKKPSVVGAVQGMITGLVCTTPAAGVQGMALVWGLASIPYTMTHLHK 343
Db 230 WTTLDVIFFGKPSVIGALQGMVGTAGVTPGAGLIQTMAAIIIGVSGTAPVASMNIHK 289
QY 344 RSKILORVDDTLGVHTHGVAGLLGGLLTGFAERTLCNLFPLVADSRGAFYGGAGQF 403
Db 290 KSAIQKVDTLAVFYTHAVAGLLGIMTGLFAHBDLVLPATRGAFYGGAGKQL 349
QY 404 GKQIAGLFVYAMNVVTSILCLAINLVLPLRMPDDKLEVDDAVHGEBAVALWMDGEM 463
Db 350 LKQLAGAFAIYAMNVVSTIILAIRVFIPLRMAEELIGDDAHGEEAVALWMDGEEK 409
QY 464 DVTKH 468
Db 410 DATRH 414

RESULT 9
US-10-953-349-10300
; Sequence 10300, Application US/10953349
; Publication No. US20060107345A1

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Query Match      39.6%; Score 1003.5; DB 6; Length 255;
Best Local Similarity 72.7%; Pred. No. 2.5e-74;
Matches 184; Conservative 24; Mismatches 44; Indels 1; Gaps 1
07      9  PLAYCGNHSASVADPLNRGDNAWOLVAATLVGLSGVPGVLYLVYGVWKKKAAVNSAFML 68
      | ||| : || ||||| ||||| ||||| : ||| : ||||| |||||

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RESULT 12
US-10-953-349-17240
; Sequence 17240, Application US/10953349
; Publication No. US20060107345A1

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; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THEREBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 17240
; LENGTH: 218
; TYPE: PRF
; ORGANISM: Glycine max
; US-10-953-349-17240

Query Match      34.8%; Score 881; DB 6; Length 218;
Best Local Similarity 72.5%; Pred. No. 1,9e-64;
Matches 158; Conservative 23; Mismatches 37; Indels 0; Gaps 0;

QY 44 VGLVVLGVGVKKKAVNSAFMALYAFPAWVICWVTAYNNSFGFKLPIWGKAPALD 103
DB 1 MEGVLILYASMYKKKAVNSAFMALYAFPAWVICWLVCHRMAGDKLPIWGKAPALG 60
QY 104 QGLVGRALPATVHYRADGSVETAAVEPLYPMATVVFQCVFAATLLILVAGSLGRMS 163
DB 61 QKFLTHRAKVPSESTHYNNGVESATSEPLPATASLVFQFTFAATLLILAGSVLGRMN 120
QY 164 FLAMNIFVPLMTFTSYTVAFAFSLMGGGLFPHNGVIDYCCGYVIHVSAGTAGTAAYWVP 223
DB 121 IKAMMAFVPLMLFSTYVGAFAFSLMGGGLFPHNGVIDYSGGYVIHLSGAGTAAWVVP 180
QY 224 RAQXDRERFPNNILFTLTGAGLLMWGMAGFNGGAPYA 261
DB 181 RLKSDRERFPNNVLMLAGLLMWGMAGFNGGAPYA 218

RESULT 13
US-10-953-349-17241
; Sequence 17241, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THEREBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 17241
; LENGTH: 208
; TYPE: PRF
; ORGANISM: Glycine max
; US-10-953-349-17241

Query Match      33.3%; Score 845; DB 6; Length 208;
Best Local Similarity 73.1%; Pred. No. 1.5e-61;
Matches 152; Conservative 21; Mismatches 35; Indels 0; Gaps 0;

QY 54 VYKKMAVNSAFMALYAFPAWVICWVTAYNNSFGFKLPIWGKAPALDQGLVGRAL 113
DB 1 MYKKMAVNSAFMALYAFPAWVICWLVCHRMAGDKLPIWGKAPALGQKFLTHRAKY 60
QY 114 PATVHYRADGSVETAAVEPLYPMATVVFQCVFAATLLILVAGSLGRMSFLAMNIFVPL 173
DB 61 PESTHYNNGVESATSEPLPATASLVFQFTFAATLLILAGSVLGRMNIRAMMAFVPL 120
QY 174 WLTFSYTVGAFAFSLMGGGLFPHNGVIDYCCGYVIHVSAGTAGTAAYWVPPRAQXDRERFP 233
DB 121 WLFTSYTVGAFAFSLMGGGLFPHNGVIDYSGGYVIHLSGAGTAAWVPPRLKSDRERFP 180
QY 234 PNNILFTLTGAGLLMWGMAGFNGGAPYA 261
DB 181 RLKSDRERFPNNVLMLAGLLMWGMAGFNGGAPYA 218
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DB 181 PNNVLLMLAGALLMWGMAGFNGGAPYA 208

RESULT 14
US-10-449-902-40126
; Sequence 40126, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40126
; LENGTH: 219
; TYPE: PRF
; ORGANISM: Oryza sativa
; US-10-449-902-40126

Query Match      30.3%; Score 769; DB 6; Length 219;
Best Local Similarity 69.0%; Pred. No. 2.4e-55;
Matches 140; Conservative 24; Mismatches 39; Indels 0; Gaps 0;

QY 19 SVADWLNKGNAMQVVAATLVGLQGVPGVLYLVYGGVKKKAVNSAFMALYAFPAWVICW 78
DB 16 AVPEWLNKGNQWQVLAATLVGLQGVPGVLYLVYGGVKKKAVNSAFMALYAFPAWVICW 75
QY 79 VTYAAYNSFGFKLPIWGKAPALDQGLVGRALPATVHYRADGSVETAAVEPLYPMAT 138
DB 76 VLAVGRMAFGDRLPIFGWKAGALTEGFLVARSVPATVHYRADGSVETAAVEPLYPMAT 135
QY 139 VYFQCVFAATLLILVAGSLGRMSFLAMNIFVPLMTFTSYTVAFAFSLMGGGLFPHNGVI 198
DB 136 WLFQCVFAATLLILVAGSLGRMSFLAMNIFVPLMTFTSYTVAFAFSLMGGGLFPHNGVI 195
QY 199 DYCCGYVIHVSAGTAGTAAYWV 221
DB 196 DYSGGYVIHLSGAGTAAWV 218

RESULT 15
US-10-471-571A-244
; Sequence 244, Application US/10471571A
; Publication No. US20060115490A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE: P026927WO
; CURRENT APPLICATION NUMBER: US/10/471,571A
; CURRENT FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: GB-0107661.1
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 5642
; SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 244
; LENGTH: 428
; TYPE: PRF
; ORGANISM: Staphylococcus aureus
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(428)
; OTHER INFORMATION: probabale ammonium
; US-10-471-571A-244
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